

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 39.6051 Seconds
(without alignments)
1795.466 Million cell updates/sec

Title: US-09-674-379A-13
Perfect score: 2533
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
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- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2533	100.0	448	19	AAW79739		Human EEGF protein
2	2533	100.0	448	20	AAW95709		Homo sapiens fetal
3	2533	100.0	448	20	AAW94281		Human extracellula
4	2533	100.0	448	21	AAAY57058		Amino acid sequenc
5	2533	100.0	448	21	AAAY54989		Full length human
6	2533	100.0	448	22	AAM93573		Human polypeptide,
7	2533	100.0	448	23	AAU75494		Human extracellula
8	2527	99.8	448	20	AAAY08063		Human EGF-like hom
9	2527	99.8	448	22	AAU29227		Human PRO polypept
10	2527	99.8	448	22	AAB31183		Amino acid sequenc
11	2527	99.8	448	24	ABU71315		Human PRO210 prote
12	2527	99.8	448	24	ABU72040		Novel human secret
13	2527	99.8	448	24	ABU65772		Human secreted/tra
14	2527	99.8	448	24	ABU66105		Novel human secret
15	2527	99.8	448	24	ABU67141		Novel human secret
16	2527	99.8	448	24	ABU67272		Novel human secret
17	2527	99.8	448	24	ABU67609		Human secreted/tra
18	2527	99.8	448	24	ABU65467		Human PRO polypept
19	2527	99.8	448	24	ABU58603		Human PRO polypept
20	2527	99.8	448	24	ABU56139		Human secreted/tra
21	2527	99.8	448	24	ABU57134		Human PRO polypept
22	2527	99.8	448	24	ABU10713		Human secreted/tra
23	2405	94.9	448	21	AAAY56750		Smooth muscle prol
24	2405	94.9	448	21	AAAY54990		Full length mouse
25	2376	93.8	461	21	AAAY56752		Smooth muscle prol
26	2376	93.8	461	21	AAAY54991		Full length mouse
27	2302	90.9	423	21	AAAY56751		Smooth muscle prol
28	2302	90.9	423	21	AAAY56753		Smooth muscle prol
29	2230	88.0	392	18	AAW31705		Human extracellula
30	1827	72.1	335	21	AAAY76008		Rat EGF extracellu
31	1827	72.1	335	22	AAB55947		Skin cell protein,
32	1827	72.1	335	23	ABB72147		Rat protein isolat
33	1289	50.9	443	18	AAW32110		Human extracellula
34	1289	50.9	443	20	AAAY16587		Extracellular prot
35	1289	50.9	443	21	AAB33418		Human PRO226 prote
36	1289	50.9	443	21	AAAY84707		A human p53 mutant
37	1289	50.9	443	21	AAAY55850		Human S1-5 ECMP-li
38	1289	50.9	443	22	AAU12330		Human PRO226 polyp
39	1289	50.9	443	23	AAU86130		Human PRO226 polyp
40	1289	50.9	443	24	ABU66728		Human PRO polypept
41	1289	50.9	443	24	ABU67004		Human secreted/tra
42	1289	50.9	443	24	ABU59809		Novel secreted and
43	1283	50.7	443	22	AAB92533		Human protein sequ
44	1282	50.6	443	21	AAAY84706		Amino acid sequenc
45	1237.5	48.9	433	21	AAB58353		Lung cancer associ

ALIGNMENTS

RESULT 1

AAW79739

ID AAW79739 standard; Protein; 448 AA.

XX

AC AAW79739;

XX

DT 25-JAN-1999 (first entry)

XX

DE Human EGF protein.

XX

KW Extracellular/epidermal growth factor-like protein; EGF; human; liver;

KW vascular smooth muscle cell proliferation; neurology; pathology; AIDS;

KW dementia; ocular; disorder; cornea; inflammation; tumour cell; kidney;

KW wound; epithelium; surgery; skin graft; ulcer; diabetic; trophic;

KW Marfan syndrome; treatment; hair follicle; embryogenesis; neoplasia;

KW epidermal cell; cancer; psoriasis; detection.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= signal

FT Protein 26..448

FT /label= EGF

FT /note= "Extracellular/epidermal growth factor-like protein"

FT Region 112..153

FT /label= EGF-1

FT Region 154..190

FT /label= EGF-2

FT Region 191..230

FT /label= EGF-3

FT Region 231..271

FT /label= EGF-4

FT Region 272..314

FT /label= EGF-5

XX

PN WO9846746-A1.

XX

PD 22-OCT-1998.

XX

PF 11-APR-1997; 97WO-US06020.

XX

PR 11-APR-1997; 97WO-US06020.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li H, Olsen HS;

XX

DR WPI; 1998-568728/48.

DR N-PSDB; AAV62432.

XX

PT New isolated extracellular/epidermal growth factor - used for

PT regulating vascular smooth muscle cell proliferation, e.g. for

PT enhancing neurological functions or treating neoplasia and other

PT disorders.

XX

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 2

AAW95709

ID AAW95709 standard; Protein; 448 AA.

XX

AC AAW95709;

XX

DT 21-JUN-1999 (first entry)

XX

DE Homo sapiens fetal kidney clone AK647 secreted protein.

XX

KW Secreted protein; fetal kidney.

XX

OS Homo sapiens.

XX

PN WO9900405-A1.

XX

PD 07-JAN-1999.

XX

PF 29-JUN-1998; 98WO-US13530.

XX

PR 30-JUN-1997; 97US-0885610.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, Mccoy JM;

PI Merberg D, Racie LA, Treacy M;

XX

DR WPI; 1999-095671/08.

DR N-PSDB; AAX07567.

XX

PT New polynucleotides encoding secreted human proteins - are derived
 PT from foetal kidney or adult retina cDNA libraries, used as, e.g.
 PT potential vaccines

XX

PS Claim 11; Pages 52-54; 76pp; English.

XX

CC The sequence is that of a secreted protein from a human fetal
 CC kidney clone AK296. Such a sequence is predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals, although no
 CC supporting data is given. Suggested activities include nutritional
 CC activity, cytokine and cell proliferation/differentiation activity,
 CC immune stimulating (e.g. as vaccines) or suppressing activity,
 CC haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, cadherin/tumour invasion suppressor activity, and tumour
 CC inhibition activity. It is also stated to be useful for gene
 CC therapy.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4e-159;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
      |||
Db    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

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      |||
Db    181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
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Qy    301 LQQTTCYNLQGGFKCIDPIRCEEPLYRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
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Db    301 LQQTTCYNLQGGFKCIDPIRCEEPLYRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
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Qy    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 3

AAW94281

ID AAW94281 standard; Protein; 448 AA.

XX

AC AAW94281;

XX

DT 07-MAY-1999 (first entry)

XX

DE Human extracellular matrix protein (ECMP)-1.

XX

KW Extracellular matrix protein; ECMP-1; diagnosis; treatment; cancer;
 KW immune disorder; human.

XX

OS Homo sapiens.

XX

PN WO9900410-A2.

XX

PD 07-JAN-1999.

XX

PF 23-JUN-1998; 98WO-US13012.

```

XX PR 27-JUN-1997; 97US-0884072.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Bandman O, Corley NC, Guegler KJ;
XX
XX DR WPI; 1999-095674/08.
XX DR N-PSDB; AAX05359.
XX
XX PT New polynucleotide encoding extracellular matrix protein, ECMP-1 -
XX PT useful in the diagnosis, prevention and treatment of immune
XX PT disorders and cancer
XX
XX PS Claim 1; Fig 1A-G; 79pp; English.
XX
XX CC This represents a human extracellular matrix protein (ECMP)-1. Host
XX CC cells containing a vector comprising the ECMP-1 nucleic acid are used
XX CC for the recombinant production of the protein. ECMP-1 and its
XX CC (ant)agonists, are useful in the diagnosis, prevention, and treatment
XX CC of cancer and immune disorders.
XX
XX SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 4e-159;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPGIKRI LTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
Db 1 MPGIKRI LTVTILALCLPSGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

QY 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
Db 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

QY 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCDTGYWLLEGQCLDIDECRYGYCQQL 180
Db 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCDTGYWLLEGQCLDIDECRYGYCQQL 180

QY 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

QY 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360

QY 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLMTRPIKGPREIQLDL 420
Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLMTRPIKGPREIQLDL 420

QY 421 EMITVNTVINFRGSSVIRLRIYVSOYPF 448

```

Db

|||||
421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 4

AAY57058

ID AAY57058 standard; Protein; 448 AA.

XX

AC AAY57058;

XX

DT 21-FEB-2000 (first entry)

XX

DE Amino acid sequence of the human secreted protein AK647.

XX

KW AK647; aortic tissue development; smooth muscle cell modulator; SCID;
KW nutritional supplement; vasculogenesis; embryonic development; infection;
KW cytokine activity; cell proliferation; cell differentiation; detect; HIV;
KW immune deficiency; haematopoiesis regulation; tissue regrowth; diagnose;
KW wound healing; restenosis; atherosclerosis; drug screen.

XX

OS Homo sapiens.

XX

PN WO9960125-A2.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US10931.

XX

PR 19-MAY-1998; 98US-0081002.

PR 21-MAY-1998; 98US-0083002.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Racie L, LaVallie E, Treacy M, Evans C;

PI Agostino M, Lu Z, Merberg D;

XX

DR WPI; 2000-053298/04.

DR N-PSDB; AAZ39892.

XX

PT Proteins, and their encoding polynucleotides, used for treating e.g.

PT smooth muscle cell growth, vasculogenesis, restenosis or

PT atherosclerosis -

XX

PS Claim 4; Page 46-47; 49pp; English.

XX

CC This is the amino acid sequence of the human secreted protein AK647. The
CC polynucleotide sequence was obtained from a human foetal kidney cDNA
CC library. AK647 homologues in chicks and rodents are involved in aortic
CC tissue development. The spatial and temporal distribution of AK647
CC indicated that it acts as an a modulator of smooth muscle cells in
CC vasculogenesis during embryonic development. The primary structure of
CC AK647 consists of multiple EGF domains. The AK647 protein can be used as
CC a nutritional source or supplement. The protein shows both inhibitory and
CC inducing, cytokine, cell proliferation and cell differentiation activity.
CC The protein may also be used in the treatment of immune deficiencies and
CC disorders, including severe combined immunodeficiency (SCID), HIV and
CC other viral, bacterial and fungal infections. Regulation of immune

XX
 AC AAY54989;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Full length human A55 protein sequence.
 XX
 KW A55 protein; human; smooth muscle proliferation; tissue generation;
 KW vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma;
 KW vascular endothelial thickening; haematopoietic cell-regulator; cytokine;
 KW percutaneous transluminal coronary angioplasty; blood coagulation; PTCA;
 KW actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
 KW tumour metastasis inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO9955864-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 28-APR-1999; 99WO-JP02284.
 XX
 PR 28-APR-1998; 98JP-0119731.
 XX
 PA (ONOEY) ONO PHARM CO LTD.
 XX
 PI Honjo T, Tashiro K, Nakamura T;
 XX
 DR WPI; 2000-038647/03.
 DR N-PSDB; AAZ40027.
 XX
 PT Novel human polypeptides for treatment of, e.g. arteriosclerosis and
 PT myoma -
 XX
 PS Claim 1; Page 76-80; 87pp; Japanese.
 XX
 CC This sequence is the human A55 protein of the invention. The protein
 CC can be used for the treatment of diseases due to abnormal proliferation
 CC of smooth muscle. The polypeptides can be used according to their inhibition
 CC of the proliferation of vascular smooth muscle cells, particularly in
 CC treating arteriosclerosis or re-narrowing by vascular endothelial
 CC thickening after percutaneous transluminal coronary angioplasty (PTCA),
 CC or myoma, haematopoietic cell-regulatory activity, cytokine activity,
 CC tissue generation/reparation activity, actin/inhibin activity, taxis
 CC and chemotaxis activity, blood coagulation/thrombotic activity,
 CC receptor/ligand activity, cadherin/tumour metastasis inhibiting activity;
 CC tumour inhibition, and as a nutrient.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4e-159;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy 61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 |||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
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 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 |||
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 |||
 Db 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
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 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 |||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 |||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 6

AAM93573

ID AAM93573 standard; Protein; 448 AA.

XX

AC AAM93573;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3357.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 7

AAU75494

ID AAU75494 standard; Protein; 448 AA.

XX

AC AAU75494;

XX

DT 23-APR-2002 (first entry)

XX

DE Human extracellular protein-like/EGF-like protein, EEGF.

XX

KW Human; extracellular protein-like protein; EGF-like;

KW protein; epidermal growth factor; EEGF; ATCC 97285; gene therapy;

KW vascular smooth muscle cell proliferation; Marfan syndrome;

KW wound healing; neurological trauma; acquired immunodeficiency syndrome;

KW AIDS-related dementia; ocular disorder; kidney disorder; liver disorder;

KW hair follicle growth promotion; burn; ulcer; corneal incision;

KW corneal inflammation; neoplasm; psoriasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= Signal_peptide

FT Protein 26..448

FT /label= Mature_EEGF

FT /note= "This region is specifically claimed in claim 10"

FT Domain 112..153

FT /label= EGF_1_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 154..190

FT /label= EGF_2_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 191..230

FT /label= EGF_3_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 231..271

FT /label= EGF_4_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 272..314

FT /label= EGF_5_domain

FT /note= "This domain is specifically claimed in claim 10"

XX

PN US2001051358-A1.

XX

PD 13-DEC-2001.

XX

PF 25-MAR-1999; 99US-0275805.

XX

PR 11-APR-1997; 97US-0839525.

PR 10-APR-1996; 96WO-US05247.

XX

PA (OLSE/) OLSEN H S.

PA (LIHH/) LI H.
 XX
 PI Olsen HS, Li H;
 XX
 DR WPI; 2002-121417/16.
 DR N-PSDB; ABK13627.
 XX
 PT New nucleic acid encoding human extracellular/epidermal growth factor,
 PT useful for diagnosis and treatment of e.g. Marfan syndrome and wounds,
 PT also related polypeptides -
 XX
 PS Claim 10; Fig 1; 22pp; English.
 XX
 CC The invention relates to a novel polynucleotide which is at
 CC least 95% identical with a sequence (ATCC 97285) encoding mature human
 CC extracellular protein-like/epidermal growth factor (EGF)-like protein,
 CC EEGF. Also included are the EEGF EGF domains, a vector containing
 CC the polynucleotide, a host cell containing the vector, anti-EEGF
 CC antibodies and antagonists of EEGF. The polynucleotide is used for
 CC recombinant production of EEGF, in gene therapy, as hybridisation probes,
 CC as antisense antagonists and for chromosome identification. The protein
 CC is used to treat patients who require EEGF, to identify specific
 CC antagonists, used to treat conditions that require inhibition of EEGF
 CC (e.g. vascular smooth muscle cell proliferation, Marfan syndrome, wound
 CC healing, neurological trauma, acquired immunodeficiency syndrome
 CC (AIDS)-related dementia, ocular disorders, kidney disorders, liver
 CC disorders, hair follicle growth promotion, burns, ulcers, corneal
 CC incisions, corneal inflammation, neoplasms and psoriasis), to raise
 CC specific antibodies and to characterise receptors. The present
 CC sequence represents EEGF.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2533; DB 23; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4e-159;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Db	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
QY	61	NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD	120
QY	121	ESNQCDVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQL	180
Db	121	ESNQCDVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYGYCQQL	180
QY	181	CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Db	181	CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
QY	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Db	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300

QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
 |||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360

QY 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 |||
 Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 |||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 8

AAAY08063

ID AAY08063 standard; Protein; 448 AA.

XX

AC AAY08063;

XX

DT 11-SEP-2000 (first entry)

XX

DE Human EGF-like homologue protein (PRO217) encoded by DNA32279 cDNA.

XX

KW Inflammatory cell infiltration; immune response; T cell proliferation;
 KW anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;
 KW T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;
 KW inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;
 KW diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;
 KW sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;
 KW skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;
 KW food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;
 KW idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
 KW EGF-like.

XX

OS Homo sapiens.

XX

PN WO9914241-A2.

XX

PD 25-MAR-1999.

XX

PF 17-SEP-1998; 98WO-US19437.

XX

PR 17-SEP-1997; 97US-0059119.

PR 18-SEP-1997; 97US-0059263.

PR 28-OCT-1997; 97US-0063550.

PR 12-NOV-1997; 97US-0065186.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066770.

PR 04-JUN-1998; 98US-0088026.

XX

PA (GETH) GENENTECH INC.

XX

PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;

XX

DR WPI; 1999-229499/19.

DR N-PSDB; AAX37670.

XX
PT Composition containing novel polypeptide PRO245, its agonist or
PT antagonist -
XX
PS Example 1; Fig 6A; 177pp; English.
XX
CC This invention describes a novel composition containing (apart from a
CC carrier or excipient), a novel PRO245 polypeptide (I), its agonist or
CC antagonist, or their fragments, for modulating: (i) infiltration of
CC inflammatory cells into tissue; (ii) an immune response; or (iii) T cell
CC proliferation. The composition increases or decreases any of the effects
CC (i)-(iii). The products of the invention have anti-inflammatory,
CC anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists
CC and their fragments, are used to treat immune-related diseases,
CC particularly T cell-mediated diseases. The diseases treated include
CC systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
CC arthritis, spondyloarthropathies, systemic sclerosis (scleroderma),
CC idiopathic inflammatory myopathies (dermatomyositis, polymyositis),
CC Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune
CC hemolytic anemia (immune pancytopenia, paroxysmal nocturnal
CC hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic
CC purpura immune-mediated thrombocytopenia), thyroiditis (Grave's disease,
CC Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic
CC thyroiditis), diabetes mellitus, immune-mediated renal disease
CC (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis,
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic
CC inflammatory demyelinating polyneuropathy, infectious hepatitis
CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, and sclerosing cholangitis, inflammatory bowel disease
CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and
CC Whipple's disease. Autoimmune or immune-mediated skin diseases including
CC bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,
CC hypersensitivity pneumonitis, and transplantation associated diseases
CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists
CC or fragment can also be used as an adjuvant in treatment of tumors.
CC Antibodies against (I) can also be used for diagnosing such diseases.
CC This sequence represents a human EGF-like homologue encoded by cDNA clone
CC DNA32279 which is described in the invention.
XX
SQ Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 20; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-159;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
Qy 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGYPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
Qy 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSTDGYWLLLEGQCLDIDECRYGYCQQL 180

Db	121	ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQL	180
Qy	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Db	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Qy	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Db	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Qy	301	LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRMDVVSGRS	360
Db	301	LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRMDVVSGRS	360
Qy	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL	420
Db	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL	420
Qy	421	EMITVNTVINFRGSSVIRLRIYVSQYPF	448
Db	421	EMITVNTVINFRGSSVIRLRIYVSQYPF	448

RESULT 9

AAU29227

ID AAU29227 standard; Protein; 448 AA.

XX

AC AAU29227;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human PRO polypeptide sequence #204.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US06520.

XX

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-602746/68.

DR N-PSDB; AAS46128.

XX

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX

PS Claim 11; Fig 408; 774pp; English.

XX

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,

CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 22; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-159;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        |||
Db      1  MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61  NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYAPPLSAPNYPTISRPLICRFGYQMD 120
        |||
Db     61  NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
        |||
Db    121  ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
        |||
Db    181  CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
        |||
Db    241  DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301  LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
        |||
Db    301  LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
        |||
Db    361  VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
        |||
Db    421  EMITVNTVINFRGSSVIRLRIYVSQYPF 448
```

RESULT 10

AAB31183

ID AAB31183 standard; Protein; 448 AA.

XX

AC AAB31183;

XX

DT 20-APR-2001 (first entry)

XX

DE Amino acid sequence of human polypeptide PRO210.

XX

KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;

KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /note= "signal peptide"
 FT Modified-site 21..27
 FT /note= "N-myristoylation site"
 FT Binding-site 54..57
 FT /note= "cell attachment site"
 FT Modified-site 64..70
 FT /note= "N-myristoylation site"
 FT Modified-site 144..156
 FT /note= "aspartic acid and asparagine hydroxylation site"
 FT Modified-site 149..155
 FT /note= "N-myristoylation site"
 FT Modified-site 186..192
 FT /note= "N-myristoylation site"
 FT Modified-site 226..232
 FT /note= "N-myristoylation site"
 FT Modified-site 242..248
 FT /note= "N-myristoylation site"
 FT Modified-site 267..273
 FT /note= "N-myristoylation site"
 FT Modified-site 283..287
 FT /note= "N-glycosylation site"
 FT Modified-site 296..300
 FT /note= "N-glycosylation site"
 FT Modified-site 310..316
 FT /note= "N-myristoylation site"
 XX
 PN WO200077037-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 22-MAY-2000; 2000WO-US14042.
 XX
 PR 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 PR 07-DEC-1999; 99US-0169495.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.

Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 |||||
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 |||||
 Db 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
 |||||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360

Qy 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 |||||
 Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 |||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 11

ABU71315

ID ABU71315 standard; Protein; 448 AA.

XX

AC ABU71315;

XX

DT 10-JUN-2003 (first entry)

XX

DE Human PRO210 protein.

XX

KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
 KW differentiation; tumour; gene therapy.

XX

OS Homo sapiens.

XX

PN US2003036143-A1.

XX

PD 20-FEB-2003.

XX

PF 02-JUL-2002; 2002US-0187600.

XX

PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.

PR	21-APR-1998;	98US-082568P.
PR	21-APR-1998;	98US-082569P.
PR	22-APR-1998;	98US-082704P.
PR	22-APR-1998;	98US-082797P.
PR	28-APR-1998;	98US-083322P.
PR	29-APR-1998;	98US-083495P.
PR	29-APR-1998;	98US-083496P.
PR	29-APR-1998;	98US-083499P.
PR	29-APR-1998;	98US-083559P.
PR	05-MAY-1998;	98US-084366P.
PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
PR	07-MAY-1998;	98US-084640P.
PR	07-MAY-1998;	98US-084643P.
PR	15-MAY-1998;	98US-085579P.
PR	15-MAY-1998;	98US-085580P.
PR	15-MAY-1998;	98US-085582P.
PR	15-MAY-1998;	98US-085700P.
PR	18-MAY-1998;	98US-086023P.
PR	22-MAY-1998;	98US-086392P.
PR	22-MAY-1998;	98US-086486P.
PR	28-MAY-1998;	98US-087098P.
PR	28-MAY-1998;	98US-087208P.
PR	02-JUN-1998;	98US-087609P.
PR	02-JUN-1998;	98US-087759P.
PR	03-JUN-1998;	98US-087827P.
PR	04-JUN-1998;	98US-088025P.
PR	04-JUN-1998;	98US-088028P.
PR	04-JUN-1998;	98US-088029P.
PR	04-JUN-1998;	98US-088033P.
PR	04-JUN-1998;	98US-088326P.
PR	05-JUN-1998;	98US-088167P.
PR	05-JUN-1998;	98US-088202P.
PR	05-JUN-1998;	98US-088212P.
PR	05-JUN-1998;	98US-088217P.
PR	09-JUN-1998;	98US-088655P.
PR	10-JUN-1998;	98US-088722P.
PR	10-JUN-1998;	98US-088738P.
PR	10-JUN-1998;	98US-088740P.
PR	10-JUN-1998;	98US-088811P.
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PR	22-JUN-1998;	98US-090252P.

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 PR 01-JUL-1998; 98US-091544P.
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 PR 02-JUL-1998; 98US-091486P.
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 PR 02-JUL-1998; 98US-091628P.
 PR 02-JUL-1998; 98US-091632P.
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Query Match 99.8%; Score 2527; DB 24; Length 448;
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QY 61 NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
 |||
 Db 61 NQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

QY 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
 |||
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

QY 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
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 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

QY 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 |||
 Db 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

QY 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360
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 Db 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360

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 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
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 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 12

ABU72040

ID ABU72040 standard; Protein; 448 AA.

XX

AC ABU72040;

XX

DT 11-JUN-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO210.

XX

KW Human; secreted and transmembrane polypeptide; PRO;

KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;

KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;

KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;

KW toxin; radiolabel; antibody; cell death; chromosome mapping;

KW gene mapping; transgenic animal; knockout animal; gene therapy;

KW tissue typing.

XX

OS Homo sapiens.

XX

PN US2002177165-A1.

XX

PD 28-NOV-2002.

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PF 01-FEB-2002; 2002US-0066500.
XX
PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 09-MAR-2000; 2000WO-US06471.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
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PR 27-OCT-1997; 97US-063329P.
PR 29-OCT-1997; 97US-063733P.
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PR 16-DEC-1997; 97US-069694P.
PR 09-FEB-1998; 98US-074086P.

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PR 28-OCT-1998; 98US-106032P.
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PR 20-JUL-1999; 99US-145070P.
PR 26-JUL-1999; 99US-145698P.
PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2003-328482/31.

DR N-PSDB; ACA60458.

XX

PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, for identifying agonists
PT or antagonists of polypeptide, and as molecular weight markers -

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PS Claim 12; Fig 10; 254pp; English.

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CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC identify other proteins or molecules involved in binding interaction.
CC The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, for generating
CC transgenic animals or knockout animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, to
CC construct hybridisation probes for mapping the gene which encodes the
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC in gene therapy, for chromosome identification and as a chromosome
CC marker. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2527; DB 24; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-159;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

QY     61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

QY    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
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Db    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

QY    181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
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Db    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRMDVVSGRS 360

QY    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
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Db    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

QY    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
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Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
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RESULT 13

ABU65772

ID ABU65772 standard; Protein; 448 AA.

XX

AC ABU65772;

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DT 19-MAY-2003 (first entry)

XX

DE Human secreted/transmembrane protein, SEQ ID 408.

XX

KW Human; PRO; secreted protein; transmembrane protein;
KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
KW cartilage disorder; sports injury.

XX

OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
XX
PR 16-SEP-1998; 98WO-US19330.
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PR 01-SEP-1999; 99WO-US20111.
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PR 05-JAN-2000; 2000WO-US00219.
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PR 01-MAR-2000; 2000WO-US05601.
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PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
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PR	07-MAY-1998;	98US-084643P.
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PR 18-AUG-1998; 98US-097022P.
 PR 26-AUG-1998; 98US-097952P.
 PR 26-AUG-1998; 98US-097954P.
 PR 26-AUG-1998; 98US-097955P.
 PR 26-AUG-1998; 98US-097971P.
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 PR 10-SEP-1998; 98US-099741P.

Query Match 99.8%; Score 2527; DB 24; Length 448;
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 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGYPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
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 Db 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

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RESULT 14

ABU66105

ID ABU66105 standard; Protein; 448 AA.

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AC ABU66105;

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DT 20-MAY-2003 (first entry)
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KW Human; secreted protein; transmembrane protein; cytostatic;
KW gene Therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003036157-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188769.
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PR 16-SEP-1998; 98WO-US19330.
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PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
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PR 15-SEP-1999; 99WO-US21090.
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PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
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PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
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PR	17-DEC-1997;	97US-069870P.
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ABU67141

ID ABU67141 standard; Protein; 448 AA.

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AC ABU67141;

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DT 28-MAY-2003 (first entry)

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KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533;
 KW PRO301; PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003;
 KW PRO6004; PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy;
 KW tumour; obesity; diabetes; insulinaemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis.

XX

OS Homo sapiens.

XX

PN US2003032062-A1.

XX

PD 13-FEB-2003.

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PF 01-FEB-2002; 2002US-0066273.

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PR 14-JUL-1998; 98WO-US14552.
 PR 10-SEP-1998; 98WO-US18824.
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 PR 16-SEP-1998; 98WO-US19330.
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PR 20-JUL-1999; 99US-145070P.
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PR 15-NOV-2001; 2001US-0002796.

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PA (GETH) GENENTECH INC.

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PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:30:17 ; Search time 15.9449 Seconds
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2533	100.0	448	4	US-09-212-168-1	Sequence 1, Appli
3	1827	72.1	335	4	US-09-312-283C-186	Sequence 186, App
4	1791	70.7	337	3	US-09-188-930-186	Sequence 186, App
5	1289	50.9	443	2	US-08-833-963C-2	Sequence 2, Appli
6	1289	50.9	443	3	US-08-980-514-1	Sequence 1, Appli
7	963.5	38.0	387	2	US-08-884-072-5	Sequence 5, Appli
8	963.5	38.0	387	2	US-08-833-963C-9	Sequence 9, Appli
9	963.5	38.0	387	3	US-08-980-514-3	Sequence 3, Appli
10	963.5	38.0	387	4	US-09-212-168-5	Sequence 5, Appli
11	912.5	36.0	274	3	US-09-188-930-336	Sequence 336, App

12	912.5	36.0	274	4	US-09-312-283C-336	Sequence 336, App
13	544	21.5	1394	6	5177197-30	Patent No. 5177197
14	521.5	20.6	575	4	US-09-482-273-159	Sequence 159, App
15	521.5	20.6	638	4	US-09-482-273-245	Sequence 245, App
16	475	18.8	638	2	US-08-897-443-1	Sequence 1, Appli
17	463	18.3	1833	3	US-08-479-722B-2	Sequence 2, Appli
18	463	18.3	1833	5	PCT-US95-02251-18	Sequence 18, Appl
19	461	18.2	1251	5	PCT-US95-02251-3	Sequence 3, Appli
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25	389.5	15.4	353	4	US-09-482-273-243	Sequence 243, App
26	377	14.9	2471	1	US-08-185-432-16	Sequence 16, Appl
27	377	14.9	2471	1	US-08-083-590A-19	Sequence 19, Appl
28	377	14.9	2471	3	US-08-532-384-19	Sequence 19, Appl
29	377	14.9	2471	4	US-08-899-232-1	Sequence 1, Appli
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32	375	14.8	810	3	US-09-273-565-34	Sequence 34, Appl
33	375	14.8	810	4	US-09-565-538-34	Sequence 34, Appl
34	375	14.8	810	4	US-09-661-468-34	Sequence 34, Appl
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38	366	14.4	816	3	US-09-273-565-37	Sequence 37, Appl
39	366	14.4	816	4	US-09-565-538-37	Sequence 37, Appl
40	366	14.4	816	4	US-09-661-468-37	Sequence 37, Appl
41	366	14.4	816	4	US-09-976-165-37	Sequence 37, Appl
42	360.5	14.2	1964	4	US-09-467-997-1	Sequence 1, Appli
43	359	14.2	2703	1	US-08-185-432-19	Sequence 19, Appl
44	359	14.2	2703	4	US-08-899-232-4	Sequence 4, Appli
45	350.5	13.8	652	2	US-08-751-305-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-884-072-1

; Sequence 1, Application US/08884072

; Patent No. 5872234

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CORNNOT01
; CLONE: 45517
US-08-884-072-1

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Query Match          100.0%; Score 2533; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.2e-193;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180
      |||
Db    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db    181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
Db    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
      |||
Db    301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

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QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 2

US-09-212-168-1

; Sequence 1, Application US/09212168
 ; Patent No. 6303765
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/212,168
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/884,072
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0333 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: CORNNOT01
 ; CLONE: 45517

US-09-212-168-1

Query Match 100.0%; Score 2533; DB 4; Length 448;
 Best Local Similarity 100.0%; Pred. No. 3.2e-193;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
        ||||||||||||||||||||||||||||
Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
  
```

RESULT 3

US-09-312-283C-186

; Sequence 186, Application US/09312283C

; Patent No. 6573095

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James G.

; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells

; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1011c2

; CURRENT APPLICATION NUMBER: US/09/312,283C

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 425

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 186

; LENGTH: 335
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-186

Query Match 72.1%; Score 1827; DB 4; Length 335;
Best Local Similarity 95.2%; Pred. No. 2.1e-137;
Matches 319; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Qy      114 RFGYQMDESNCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECR 173
          |||
Db      1  RFGYQMDEGNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECR 60

Qy      174 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
          |||
Db      61 YGYCQQLCANVPGSYSCTCNPGFTLNDDGRSCQDVNECETENPCVQTCVNTYGSFICRCD 120

Qy      234 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 293
          |||
Db      121 PGYELEEDGIHCSMDDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLEDNRSCQDINECE 180

Qy      294 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPLYRISDNRCMCPAENPGCRDQPFILYRDM 353
          |||
Db      181 HRNHTCTPLQTCYNLQGGFKCIDPIVCEEPLYLLIGDNRCMCPAENTGCRDQPFILFRDM 240

Qy      354 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 413
          |||
Db      241 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 300

Qy      414 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
          |||
Db      301 RDIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 335
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RESULT 4

US-09-188-930-186
; Sequence 186, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 186
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: UNSURE

US-09-188-930-186

Matches 314; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 414 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448

; COUNTRY: USA


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; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,963C
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/05033
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF258
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-963C-2

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```

Query Match          50.9%; Score 1289; DB 2; Length 443;
Best Local Similarity 49.9%; Pred. No. 1.3e-94;
Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

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Qy      1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
      :|| : : :| | || ::: :||:|:| | | | :||| :|
Db      8 LPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDLPDSQHCRDVNECLTIPEACKG 67

Qy     56 DMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRF 115
      :| |:| ||||:|:| : | : || | || | |
Db     68 EMKCINHYGGYLCLPRSAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP 111

Qy    116 GYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQCLDIDECRYG 175
      ||: |: : ||||| | | |:| | | | |:| ||| : :|:| |||||
Db    112 GYEPDDQDSCVDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171

Qy    176 YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
      ||| | |:|:| : | ||| | : ||| |||| | | | |:|:|:| ||| |
Db    172 YCQHRCVNLPGSFRQCCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG 231

Qy    236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
      ||| || |||:|:|:| :|:|: ||:| | : | || | || | | |||:|
Db    232 YELHRDGFSCSDIDECSYSSYLQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECESG 290

Qy    296 NHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITLYRDMDV 355
      | |: ||| | ||:|:| || |||:|:|:|:| ||| || |:| | :|:| | :
Db    291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSI VHRMTI 350

Qy    356 VSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 415

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      | | | | | : | | : | | : | | | | | | | | : | | : | | : | | : | | | |
Db    351 TSERSVPADV FQIQATSVYPGAYNAFQIRAGNSQGD FYIRQINNVSAMLV LARPVTGP RE 410

QY    416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      | | | | | : | | : | | : | | | | | | | | : | | : | | : | | : | | | |
Db    411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443

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RESULT 6

US-08-980-514-1

; Sequence 1, Application US/08980514

; Patent No. 6004753

; GENERAL INFORMATION:

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT

; TITLE OF INVENTION: EIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,514

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0436 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 443 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BRSTNOT13

; CLONE: 2786449

US-08-980-514-1

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Query Match          50.9%;  Score 1289;  DB 3;  Length 443;
Best Local Similarity 49.9%;  Pred. No. 1.3e-94;

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Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

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Qy      1 MPGIKRIITVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
      :|| : : :| | || : : : || : : : | | | : : || ||||| :|
Db      8 LPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSDQHCRDVNECLTIPEACKG 67

Qy     56 DMMCVNQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRF 115
      :| | :| ||||| :|| : | : || | || || |
Db     68 EMKCINHYGGYLCLPRSAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP 111

Qy    116 GYQMDSESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGWYLLLEGQCLDIDECRYG 175
      || : : : ||||| || | :| | | | | :| ||| : : : |||||
Db    112 GYEPDDQDSCVDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171

Qy    176 YCQQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
      ||| | :||| : | | ||| | : ||| |||| | || | | :|| :||| |
Db    172 YCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG 231

Qy    236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPPTYFCSCPPGYILLDDNRSCQDINECEHR 295
      ||| || ||| :||| :| :||| : ||| : | || || | | |||| :|||
Db    232 YELHRDGFSCSDIDECSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECESG 290

Qy    296 NHTCNLQQTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFTILYRDMDV 355
      | | : ||| | || :||| || |||| :|| :||| || ||| :||| :| :
Db    291 AHQCSEAQTCVNFHGGYRCVDTNRCVEFYIQVSENRLCPASNPLCREQPSSIVHRYMTI 350

Qy    356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 415
      | ||||| :|| :||| : |||| | || :|| :||| :|| ||| :|||
Db    351 TSERSVPADVFOIQATSVYPGAYNAFQIRAGNSQGDYFIRQINNVSAMLVLARPVTGPRI 410

Qy    416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      ||||| :|| :||| :||| ||| :|| | |
Db    411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443
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RESULT 7

US-08-884-072-5

; Sequence 5, Application US/08884072

; Patent No. 5872234

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0


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; Sequence 9, Application US/08833963C
; Patent No. 5916769
; GENERAL INFORMATION:
;   APPLICANT: Olsen, et al.
;   TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
;   TITLE OF INVENTION: HCABA58X
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Ave
;     CITY: Rockville
;     STATE: MD
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/833,963C
;     FILING DATE: 11-APR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/US96/05033
;     FILING DATE: 10-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Brookes, A. Anders
;     REGISTRATION NUMBER: 36,373
;     REFERENCE/DOCKET NUMBER: PF258
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 301-309-8504
;     TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 387 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-833-963C-9

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Query Match          38.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 7.3e-69;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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QY      96 APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      | |  | : |  | : |  ||: | | |  | : | |  | : | |  | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

QY     156 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      ||  ||  ||: || || |  || | |  ||: |  | : || |  | : || |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFGQLAANNYTQVDINECDAS 155

QY     215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 274
      | | | | |  || || | : | || |  | : |  | : || |  | : || | : || |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

```

QY 275 PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMC 334
 || :: :|:||||||| | | : |:| |||:| |::||: . :|||:|
 Db 216 QGYQVV-RSRTCQDINECETTNE-CREDEM CWN YHGGFR CYPRNPCQDPYILTPENRCVC 273
 QY 335 PAENPGCRDQPFITILYRDM DVVSGRSVPADIFQM QATTRYPGAYYIFQIKSGNEGREFYM 394
 | | ||: | :|:|: | : | |||:||||:|||| | |::||| | ||:
 Db 274 PVSNAMELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL 333
 QY 395 RQTGPISATLVMTRPIKGP REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||| |:| | |: : : |||| :|||:|:|:| || |||:| | | : |
 Db 334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387

RESULT 9

US-08-980-514-3

; Sequence 3, Application US/08980514

; Patent No. 6004753

; GENERAL INFORMATION:

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT

; TITLE OF INVENTION: EIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,514

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0436 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 387 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank
; CLONE: 458228
US-08-980-514-3

Query Match 38.0%; Score 963.5; DB 3; Length 387;
Best Local Similarity 48.3%; Pred. No. 7.3e-69;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```
Qy      96 APPLSAPNYPTISRPLICRFGYQMDSESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      | | | | : | | : | ||: | | | | : || | | : || | | : | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLEGQCCLDIDECRY-GYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATE 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQSPGFQLAANNYTCVDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      156 NQCAQQCYNILGSFICQCNCQGYELSSDRLNCEIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy      275 PGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDPIRCEEPLYLRISDNRCMC 334
      | | : : : | | | | | | | | | | | | | | | | | | | | | |
Db      216 QGYQVV-RSRTCQDINECETTNE-CREDEMCCWNYHGGFRCPYPRNPCQDPYILTPENRCVC 273

Qy      335 PAENPGCRDQPFITLYRDMDDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      274 FVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGGEFYL 333

Qy      395 RQTGPISATLVMTTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      | | | | : | | | | : : | | | | : | | | | : | | | | : | |
Db      334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFPSF 387
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RESULT 10

US-09-212-168-5

; Sequence 5, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/884,072
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-09-212-168-5

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Query Match          38.0%; Score 963.5; DB 4; Length 387;
Best Local Similarity 48.3%; Pred. No. 7.3e-69;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      96 APPLSAPNYPTISRPLICRFGYQMDSESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy      156 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCDINECDAS 155

Qy      215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCP 274
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      156 NQCAQQCYNILGSFICQCNGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKPFSCMCP 215

Qy      275 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMC 334
      | | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      216 QGYQVV-RSRTCQDINECETTNE-CREDEMWNHGGFRCPYPRNPCQDPYILTPENRCVC 273

Qy      335 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
      | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      274 PVSNAMELELPQSIVYKYMSIRSDRSVPDIFQIQATTIYANTINTFRIKSGNENGFEYL 333

Qy      395 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      334 RQTSFVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPPFSF 387

```

```

RESULT 11
US-09-188-930-336
; Sequence 336, Application US/09188930A
; Patent No. 6150502

```



```
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 336
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-336
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Query Match          36.0%; Score 912.5; DB 3; Length 274;
Best Local Similarity 56.0%; Pred. No. 5.5e-65;
Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;
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```
Qy      174 YGYCQQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
      | ||| | | :|||: | | ||| | : ||| |||| | | | | | :|||:|
Db      1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy      234 PGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 293
      |||| | | |||:||||:| :|||: |||:| | : | || | | | | | ||||:|
Db      61 QGYELHRDGFSCSDIDECSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119

Qy      294 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFITLYRDM 353
      | | : ||| | | |||:| | | |||:| :|||:| | | |||:| | :|:| |
Db      120 SGAHQCSQAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSI VHRYM 179

Qy      354 DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 413
      : | |||||:|:|:|: |||| | |||:| | :||:| | :| |||:| |
Db      180 TITRSVSPADVFPQIQATSVYPGAYNAFQIRAGNSQGDYFI RQINNVSAMLVLARPV TGP 239

Qy      414 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      || |||||:|:|:|:| |||:| | :| | |
Db      240 REYVLDLEMVTMNSLMSYRASSVLRLTVFVGAYTF 274
```

RESULT 12

```
US-09-312-283C-336
; Sequence 336, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
```

; FILE REFERENCE: 11000.1011c2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 336
 ; LENGTH: 274
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-312-283C-336

Query Match 36.0%; Score 912.5; DB 4; Length 274;
 Best Local Similarity 56.0%; Pred. No. 5.5e-65;
 Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

Qy 174 YGYCQQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 233
 | || | | : || | | | : || | || | | | | | | | | : || | : || |
 Db 1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60
 Qy 234 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 293
 || | | | | | : || | : || | : || | : || | : || | | | | | | | | : || |
 Db 61 QGYELHRDGFSCSDIDECSYSSYLCCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119
 Qy 294 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFILYRDM 353
 | : || | | | : || : || | | | : || | : || | : || | : || | : || |
 Db 120 SGAHQCSQAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSI VHRYM 179
 Qy 354 DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 413
 : | || | | | : || : || | | | | | : || : || | : || | : || | : || |
 Db 180 TITERSVPADVFQIQATSVYPGAYNAFQIRAGNSQGDYIRQINNVSAMLVLARPVTPG 239
 Qy 414 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 || || | | : || : || : || : || : || : || : || : || : || : || : ||
 Db 240 REYVLDLEMTMNSLSYRASSVLRLTVFVGAYTF 274

RESULT 13
 5177197-30

; Patent No. 5177197
 ; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
 ; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAEISSON-WELSH,
 ; LENA; HELDIN, CARL-HENRIK
 ; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
 ; HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN
 ; NUMBER OF SEQUENCES: 53
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/487,343
 ; FILING DATE: 27-FEB-1990
 ; SEQ ID NO: 30:
 ; LENGTH: 1394
 5177197-30

Query Match 21.5%; Score 544; DB 6; Length 1394;
 Best Local Similarity 29.4%; Pred. No. 5.5e-35;
 Matches 128; Conservative 52; Mismatches 134; Indels 122; Gaps 17;

Qy 16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75

Db 562 CINLPVRYTCICYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSF LCI----- 614
 Qy 76 YRGYPYSPYSTPYSGPYPAAPPLSAPNYPTISRPLI-----CRFGYQ 118
 Db 615 -----CPAGFMASEEGTNCIDVDECLRPDVCGBGHCVNTVGAFRCEYCD SGYR 662
 Qy 119 MDESNQCVDVDECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGY 176
 Db 663 MTQRGRCEDIDECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLPNV 720
 Qy 177 CQQ-LCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- 219
 Db 721 CANGDCSNLEGSYMC SCHKGYTRTPDHKHC RDI DECQQGNLCVNGQCKNTEGSFRCTCGQ 780
 Qy 220 -----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF 253
 Db 781 GYQLSAAKDQCEDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCE DINECLE 840
 Qy 254 SEFLCQH-ECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQT CYNLQGGF 312
 Db 841 DKSVCQRGDCINTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSF 898
 Qy 313 KCI-----DPIRCEEPYLRIS-----DN-----RCMC-----PAENPGCR 342
 Db 899 HCVCQQGFSISADGRTCEDIDECVNNTVCD SHGFC DNTAGSFRCLCYQGFQAPQDQGQCV 958
 Qy 343 DQPFTILYRDMDVVSG 358
 Db 959 D-----VNECELLSG 968

RESULT 14

US-09-482-273-159

; Sequence 159, Application US/09482273

; Patent No. 6534631

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 71 Human Secreted Proteins

; FILE REFERENCE: PZ030P1

; CURRENT APPLICATION NUMBER: US/09/482,273

; CURRENT FILING DATE: 2000-01-13

; EARLIER APPLICATION NUMBER: PCT/US99/15849

; EARLIER FILING DATE: 1999-07-14

; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,922

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,956

; EARLIER FILING DATE: 1998-07-15

; NUMBER OF SEQ ID NOS: 267

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 159

; LENGTH: 575

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-482-273-159

Query Match 20.6%; Score 521.5; DB 4; Length 575;
 Best Local Similarity 29.4%; Pred. No. 1.2e-33;
 Matches 144; Conservative 58; Mismatches 164; Indels 123; Gaps 21;

```

Qy      13 LALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCPRT 72
      || | : | : | ||: || | | : || | || | | : |
Db      157 LATALQAEEN-EVGCPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDC 215

Qy      73 NPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECA 132
      | | : : | || | |
Db      216 GP-----GFRVADGAGCEDVDECL 234

Qy      133 TDSHCNPTQICINTEGGYTCSCTDGYWLLEG---QCLDIDECRY--GYCQQLCANVPGS 187
      | : | : | || | : || | || : | | | : | | | : |
Db      235 EGLDDCHYNQLCENTPGGHRCS CPRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGS 293

Qy      188 YSCTCNPGFTLNEDGRSC-----QDVNECATENPCV-----QTCVNTYGSFI---- 229
      | | | || | | || : | | : | : | : | : | : |
Db      294 YRCLCPPGQTLLRDGKACTSLERNQGQNTTVSHRGPLLPLWLRPWASIPGTSYHAWVSLRP 353

Qy      230 -----CRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYIL 279
      | || : : : || | : || | | || | | | | | |
Db      354 GPMALSSVGRAWCPPGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRL 410

Qy      280 LDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPA--- 336
      | : || || || || : | | | : | : | : | | |
Db      411 LPSGKNCQDINECEEESI ECGPGQMCFNTRGSYQCVD-----TPCPATYR 455

Qy      337 --ENPG-----CRDQ-----PFTILYRMDVVSGRSVPADIFQMATTR--YPGAYYIFQ 382
      : || | | | : | | : : | | : : | : |
Db      456 QGSPSGTCFRRCSSQDCGTGGPSTLQYRLPLPLGVRAHHDVARLTA FSEVGVPANRTELS 515

Qy      383 IKSGNEGREFYMRQTGPISATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRL 439
      : : | : | | | | | : : | : | | | |
Db      516 MLEPDRSPFALR---PLRAGLGAVYTR-----RALTRAGLYRLTVRAAAP-RHQSVFVL 566

Qy      440 RIYVSQYPF 448
      | || || :
Db      567 LIAVSPYPY 575
  
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RESULT 15

US-09-482-273-245

; Sequence 245, Application US/09482273
 ; Patent No. 6534631
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: PZ030P1
 ; CURRENT APPLICATION NUMBER: US/09/482,273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,922

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; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-245
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Query Match          20.6%; Score 521.5; DB 4; Length 638;
Best Local Similarity 29.4%; Pred. No. 1.4e-33;
Matches 144; Conservative 58; Mismatches 164; Indels 123; Gaps 21;
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```
Qy      13 LALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRT 72
      || | : | : | ||: || | | : | : || | || | | | : |
Db      220 LATALQAEEN-EVGCPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDC 278

Qy      73 NPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDSESNQCVDVDECA 132
      | | : : | | | | |
Db      279 GP-----GFRVADGAGCEDVDECL 297

Qy      133 TDSHQCNPTQICINTEGGYTCSCTDGYWLLEG---QCLDIDECRY--GYCQQLCANVPGS 187
      | : | : | || ||: || | || : | | | : | | | : | |
Db      298 EGLDDCHYNQLCENTPGGHRCS CPRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGS 356

Qy      188 YSCTCNPFGFTLNEDGRSC-----QDVNECATENPCV-----QTCVNTYGSFI---- 229
      | | | | | | | | : | | : | : | : | : | : |
Db      357 YRCLCPPGQTLLRDGKACTSLERNQNVTTVSHRGPLLPWLRPWASIPGTSYHAWVSLRP 416

Qy      230 -----CRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYIL 279
      | | : : : | | | : | | | | | | | | | | | |
Db      417 GPMALSSVGRAWCPPGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRL 473

Qy      280 LDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPA--- 336
      | : | | | | | | : | | | : | : | : | | |
Db      474 LPSGKNCQDINECEEESIECGPGQMCFNTRGSYQCVD-----TPCPATYR 518

Qy      337 --ENPG-----CRDQ-----PFTILYRDMDVVSGRSVPADIFQMQATTR--YPGAYYIFQ 382
      : || | | | | | | : | | : : | | : : | : |
Db      519 QGPSPGTCFRRCSDQDCGTGGPSTLQYRLPLPLGVRAHHDVARLTAFSEVGVPANRTELS 578

Qy      383 IKSGNEGREFYMRQTGPISATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRL 439
      : : | : | | | | | | : : | : | | | |
Db      579 MLEPDPRSPFALR---PLRAGLGAVYTR-----RALTRAGLYRLTVRAAAP-RHQSVFVL 629

Qy      440 RIYVSQYPF 448
      | | | |
Db      630 LIAVSPYPY 638
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Search completed: January 9, 2004, 12:35:35
Job time : 17.9449 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:34:12 ; Search time 29.8324 Seconds
(without alignments)
3026.121 Million cell updates/sec

Title: US-09-674-379A-13
Perfect score: 2533
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	2533	100.0	448	9	US-09-083-002-2	Sequence 2, Appli
2	2533	100.0	448	9	US-09-275-805-2	Sequence 2, Appli
3	2533	100.0	448	9	US-09-836-561-1	Sequence 1, Appli
4	2533	100.0	448	14	US-10-041-016-2	Sequence 2, Appli
5	2527	99.8	448	12	US-10-199-672-408	Sequence 408, App
6	2527	99.8	448	12	US-10-187-749-408	Sequence 408, App
7	2527	99.8	448	12	US-10-194-457-408	Sequence 408, App
8	2527	99.8	448	12	US-10-184-642-408	Sequence 408, App
9	2527	99.8	448	12	US-10-196-747-408	Sequence 408, App
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19	2527	99.8	448	12	US-10-174-583-408	Sequence 408, App
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39	2527	99.8	448	12	US-10-179-508-408	Sequence 408, App
40	2527	99.8	448	12	US-10-179-512-408	Sequence 408, App
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42	2527	99.8	448	12	US-10-066-198-15	Sequence 15, Appl
43	2527	99.8	448	12	US-10-173-702-408	Sequence 408, App
44	2527	99.8	448	12	US-10-173-703-408	Sequence 408, App
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ALIGNMENTS

RESULT 1
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 ; Sequence 2, Application US/09083002
 ; Patent No. US20010016650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth

; APPLICANT: McCoy, John M.
 ; APPLICANT: Racie, Lisa A.
 ; APPLICANT: LaVallie, Edward R.
 ; APPLICANT: Merberg, David
 ; APPLICANT: Treacy, Maurice
 ; APPLICANT: Evans, Cheryl
 ; APPLICANT: Agostino, Michael
 ; APPLICANT: Lu, Zhijian
 ; APPLICANT: Honjo, Tasuku
 ; APPLICANT: Tashiro, Kei
 ; APPLICANT: Nakamura, Tomoyuki
 ; TITLE OF INVENTION: SECRETED PROTEINS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/083,002
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sprunger, Suzanne A.
 ; REGISTRATION NUMBER: P-41,323
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8284
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-083-002-2

Query Match 100.0%; Score 2533; DB 9; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.9e-192;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-275-805-2

; Sequence 2, Application US/09275805

; Patent No. US20010051358A1

; GENERAL INFORMATION:

; APPLICANT: OLSEN, HENRIK S.

; APPLICANT: LI, HAODONG

; TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL GROWTH FACTOR

; TITLE OF INVENTION: LIKE PROTEIN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/275,805

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/839,525

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: BROOKES, ANDERS A.

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF224

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8509
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 448 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-275-805-2

Query Match 100.0%; Score 2533; DB 9; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.9e-192;
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Db    121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

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RESULT 3

US-09-836-561-1

; Sequence 1, Application US/09836561

; Patent No. US20020038006A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Corley, Neil C.

; Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

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; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/836,561
;   FILING DATE: 16-Apr-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/212,168
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 448 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;     LIBRARY: CORNNOT01
;     CLONE: 45517
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-836-561-1

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Query Match          100.0%; Score 2533; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.9e-192;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

QY    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
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Db    121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

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 Db 241 |||||DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 Qy 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
 Db 301 |||||LQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
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 Db 361 |||||VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
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 Db 421 |||||EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 4

US-10-041-016-2

; Sequence 2, Application US/10041016

; Publication No. US20020165151A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
 ; McCoy, John M.
 ; Racie, Lisa A.
 ; LaVallie, Edward R.
 ; Merberg, David
 ; Treacy, Maurice
 ; Evans, Cheryl
 ; Agostino, Michael
 ; Lu, Zhijian
 ; Honjo, Tasuku

TITLE OF INVENTION: SECRETED PROTEINS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/041,016
 FILING DATE: 07-Jan-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/083,002
 FILING DATE: 21-MAR-1998

ATTORNEY/AGENT INFORMATION:


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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-408

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Query Match          99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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         |||

Qy      61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
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Db      61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
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Qy      121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

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Db	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Qy	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Db	241	DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Qy	301	LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS	360
Db	301	LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS	360
Qy	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL	420
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RESULT 6

US-10-187-749-408

; Sequence 408, Application US/10187749

; Publication No. US20030153036A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/187,749

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US/10/052,586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

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; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-749-408

```

```

Query Match          99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420

Qy    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

```

RESULT 7

US-10-194-457-408

; Sequence 408, Application US/10194457

; Publication No. US20030153037A1


```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-408

```

```

Query Match          99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        |||
Db       1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        |||

QY      61 NQGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
        |||
Db       61 NQGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
        |||

```

Qy 121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDDGYWLLEGQCLDIDECRYGYCQQL 180
 |||
 Db 121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDDGYWLLEGQCLDIDECRYGYCQQL 180
 Qy 181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 |||
 Db 181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 |||
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 Qy 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRMDVVSGRS 360
 |||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRMDVVSGRS 360
 Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 |||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 |||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 8

US-10-184-642-408

; Sequence 408, Application US/10184642

; Publication No. US20030157635A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194

; CURRENT APPLICATION NUMBER: US/10/184,642

; CURRENT FILING DATE: 2002-06-27

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-642-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy 61 NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy 181 CANVPGSYSCTCNPGLTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CANVPGSYSCTCNPGLTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 9

US-10-196-747-408

; Sequence 408, Application US/10196747

; Publication No. US20030162250A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C346

; CURRENT APPLICATION NUMBER: US/10/196,747

; CURRENT FILING DATE: 2002-07-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-747-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
      |||
Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSNFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
      |||
Db     61 NQNGGYLCIPRTNPVYRGYPYSNFYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
      |||
Db    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
      |||
Db    181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
      |||
Db    241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
      |||
Db    301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
      |||
Db    361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420

Qy    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
      |||
Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
```

RESULT 10

US-10-173-689-408

; Sequence 408, Application US/10173689

; Publication No. US20030166104A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C10
 ; CURRENT APPLICATION NUMBER: US/10/173,689
 ; CURRENT FILING DATE: 2002-06-17
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 408
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-173-689-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPGIKRIILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MPGIKRIILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

QY 61 NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD 120

QY 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

QY 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

QY 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360

QY 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420

QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 11

US-10-173-690-408

; Sequence 408, Application US/10173690

; Publication No. US20030166105A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C9
 ; CURRENT APPLICATION NUMBER: US/10/173,690
 ; CURRENT FILING DATE: 2002-06-17
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 408
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-173-690-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

 QY 61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

 QY 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ESNQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

 QY 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

 QY 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

 QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS 360

 QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420

 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 12

US-10-173-691-408

; Sequence 408, Application US/10173691

; Publication No. US20030166106A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C13

; CURRENT APPLICATION NUMBER: US/10/173,691

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-691-408

Query Match 99.8%; Score 2527; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 5.7e-192;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRLTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
| | | | |
Db 1 MPGIKRLTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy 61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120
| | | | |
Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180
| | | | |
Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
| | | | |
Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
| | | | |
Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

QY 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRS 360
 QY 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 13

US-10-173-692-408

; Sequence 408, Application US/10173692
 ; Publication No. US20030166188A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C20
 ; CURRENT APPLICATION NUMBER: US/10/173,692
 ; CURRENT FILING DATE: 2002-06-17
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 408
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-173-692-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 5.7e-192;
 Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 QY 61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYAPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYAPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 QY 121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 301 LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDM DVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQOTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDM DVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 361 VPADIFQM QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQM QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||||||||||||||||

RESULT 14

US-10-173-694-408

; Sequence 408, Application US/10173694

; Publication No. US20030166107A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C19

; CURRENT APPLICATION NUMBER: US/10/173,694

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-694-408

Query Match 99.8%; Score 2527; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 5.7e-192;

Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
 QY 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMD 120
 QY 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQL 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQL 180
 QY 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 CANVPGSYSCTCNPFGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
 QY 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 DGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
 QY 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFITILYRDMDVVSGRS 360
 QY 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
 QY 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||||||||||||||||||||||||||||||||||||||
 Db 421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 15

US-10-173-698-408

; Sequence 408, Application US/10173698

; Publication No. US20030166108A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C12

; CURRENT APPLICATION NUMBER: US/10/173,698

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien
US-10-173-698-408

Query Match 99.8%; Score 2527; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 5.7e-192;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV 60

Qy     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 NQNGGYLCIPRTNPVYRGYPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD 120

Qy    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ESNQCVDVDECATDSHQCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQL 180

Qy    181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CANVPGSYSTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE 240

Qy    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN 300

Qy    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360

Qy    361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDL 420

Qy    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
        ||||||||||||||||||
Db    421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
```

Search completed: January 9, 2004, 12:43:58
Job time : 30.8324 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:29:16 ; Search time 16.9736 Seconds
(without alignments)
2538.270 Million cell updates/sec

Title: US-09-674-379A-13
Perfect score: 2533
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1109.5	43.8	493	2	JC5621		epidermal growth f
2	963.5	38.0	387	2	I38449		extracellular prot
3	746	29.5	685	2	S78040		fibulin, splice fo
4	737	29.1	683	2	C36346		fibulin 1 precurs
5	733.5	29.0	1221	2	A49457		fibulin-2 precurs
6	709.5	28.0	1184	2	A55184		fibulin-2 precurs
7	703.5	27.8	705	2	S34968		fibulin, splice fo
8	619	24.4	601	2	B36346		fibulin 1 precurs
9	606.5	23.9	689	2	T42760		fibulin, splice fo
10	599.5	23.7	712	2	T42990		fibulin 1, splice
11	596	23.5	589	2	T43210		fibulin-1D precurs
12	577.5	22.8	798	2	T22793		hypothetical prote
13	544	21.5	1394	2	A35626		transforming growt

14	532.5	21.0	3002	2	A47221	fibrillin 1 precur
15	531.5	21.0	2871	2	A55567	fibrillin I - bovi
16	523	20.6	1712	2	A38261	masking protein pr
17	518.5	20.5	2871	2	A55624	fibrillin-1 precur
18	518.5	20.5	2907	2	A57278	fibrillin-2 precur
19	517.5	20.4	2918	2	A54105	fibrillin-2 precur
20	480.5	19.0	1820	2	A55494	latent transformin
21	475	18.8	741	2	T46488	hypothetical prote
22	461	18.2	1251	2	A57293	latent transformin
23	459	18.1	1620	2	T27283	hypothetical prote
24	444	17.5	1574	2	T13954	MEGF6 protein - ra
25	392	15.5	886	2	A57172	probable hormone r
26	388	15.3	3507	2	T34513	hypothetical prote
27	372.5	14.7	1106	2	T18739	hypothetical prote
28	371.5	14.7	2471	2	A49128	cell-fate determin
29	365.5	14.4	1203	2	A49175	Motch B protein -
30	364	14.4	810	2	T10756	Nel-homolog protei
31	361	14.3	1081	2	T31329	receptor tyrosine
32	359.5	14.2	1964	2	T09059	notch4 - mouse
33	359	14.2	511	2	T17298	hypothetical prote
34	358	14.1	2555	2	A40043	notch protein homo
35	356	14.1	2703	1	A24420	notch protein - fr
36	355.5	14.0	2437	2	S42612	transmembrane prot
37	346	13.7	1064	2	A40136	fibropellin Ia - s
38	346	13.7	2524	2	A35844	Xotch protein - Af
39	344	13.6	2321	2	S78549	notch3 protein - h
40	340.5	13.4	673	2	A48089	growth arrest-spec
41	337.5	13.3	2318	2	S45306	notch 3 protein -
42	337.5	13.3	2531	2	S18188	notch protein homo
43	337	13.3	2531	2	T31070	notch homolog - se
44	335.5	13.2	674	2	I55476	growth potentiatin
45	335	13.2	2531	2	A46019	notch-1 protein -

ALIGNMENTS

RESULT 1

JC5621

epidermal growth factor-like protein, T16 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C;Accession: JC5621

R;Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S. Biochem. Biophys. Res. Commun. 237, 245-250, 1997

A;Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5).

A;Reference number: JC5621; MUID:97415782; PMID:9268694

A;Accession: JC5621

A;Molecule type: mRNA

A;Residues: 1-493 <OZA>

A;Cross-references: DDBJ:D89730; NID:g2429082; PIDN:BAA22265.1; PID:d1023127; PID:g2429083

C;Comment: This protein plays a role in the regulation of cell growth by interacting with DAN protein through DA41 protein.

C;Keywords: glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

F;28-70,158-199,200-237,238-277,278-318,319-359/Region: epidermal growth factor-like repeat

F;249/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 43.8%; Score 1109.5; DB 2; Length 493;
Best Local Similarity 42.3%; Pred. No. 1.5e-65;
Matches 206; Conservative 73; Mismatches 161; Indels 47; Gaps 5;

```
Qy      7 ILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGY 66
      :||: :: : |||:|:: | || |||| :|:|:| | ||| |||
Db      9 MLTLALVKSQVTEETITYTQCTDGYEWDVPVRQQCKDIDECDIVPDACKGGMKCVNHYGGY 68

Qy     67 LCIPRTNPVYRGPYSNPYSTPYS-----GPYPAAAPPLSAP 102
      ||:|:| : || : | : |:| : : |
Db     69 LCLPKTAQIIVNNEQPQQETPAAEASSGAATGTIAARSMATSGVI PGGGFIASATAVAGP 128

Qy    103 NYPT-----ISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQ 142
      | : | ||: | | | |:| | : : | |
Db    129 EVQTGRNNFVIRRNFPADPQRI PSNP SHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQ 188

Qy    143 ICINTEGGYTCSCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNED 201
      :||| | :|| | || ||:|||| | | | | | |:| | ||||| | :
Db    189 VCINLRGSFTCHCLPGYQKRGEQCVDIDEC SVPPYCHQGC VNTPGSFYCQCNPGFQLAAN 248

Qy    202 GRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHE 261
      :| |:| | | | | | ||||:|: |||| | :| |:| | | :|||:|
Db    249 NYTCVDINECDASNQCAQQCYNILGSFICQCNOGYELSSDRLNCEDIDECRTSSYLCQYQ 308

Qy    262 CVNQPGTYFCSCPPGYIILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCE 321
      |||:| | : | | | | : : |:| ||||| | | : |:| |||:| | :
Db    309 CVNEPGKFSCMCPQGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPQNPCQ 366

Qy    322 EPYLRISDNRCMCPAENPGCRDQPF TILYRDM DVVSGRSVPADIFQM QATTRYPGAYYIF 381
      :||: |:|:| | | ||| | :|:|: |:| | |||:| | |:| | |
Db    367 DPYVLTSENRCVCPVSNTMCRDVPQSI VYKYMNI RSDRSVPSDIFQIQATTIYANTINTF 426

Qy    382 QIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI 441
      :||| | | |:| | |:| | | : : ||| : |:|:|:|: || |:| |
Db    427 RIKSGNENGEFYLRQTS PVSAMLV LKSLTGP REHIVGLEMLTVSSIGTFRTSSVLRLTI 486

Qy    442 YVSQYPF 448
      | : |
Db    487 IVGPFSF 493
```

RESULT 2

I38449

extracellular protein - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I38449

R;Lecka-Czernik, B.; Lumpkin, C.K.

Mol. Cell. Biol. 15, 120-128, 1995

A;Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts encoding a novel protein in the epidermal growth factor-like repeat family stimulates DNA synthesis.

A;Reference number: I38449; MUID:95097983; PMID:7799918

A;Accession: I38449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C;Genetics:
A;Gene: S1-5

Query Match 38.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 4.4e-56;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```
Qy      96 APPLSAPNYPTISRPLICRFGYQMDSESNQCVDVDECATDSHQCNPTQICINTEGGYTCSC 155
      | |  | : | |  : | ||: | | | |:| | | :| | | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     156 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 214
      ||  ||:| | | | | | | | | | | | | | : : | | :| | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQSPGFQLAANNYTCVDINECDAS 155

Qy     215 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 274
      | | | | | | | | | | | | | | : | | | | | | | | : | | |
Db     156 NQCAQQCYNILGSFICQCNOGYELSSDRLNCEIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     275 PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 334
      || : : : | | | | | | | | | | | | : | | | | | | | | : | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMWNHYHGGFRCYPRNPCQDPYILTPEINRCVC 273

Qy     335 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 394
      | | | | | : | : | : | : | | | | | | | | | | | | | | : | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL 333

Qy     395 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
      || | | : | | | | : : | | | | : | | | | | : : | | | | | | : |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
```

RESULT 3

S78040

fibulin, splice form C precursor - mouse

N;Alternate names: basement-membrane protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Aug-2002

C;Accession: S78040; S78560; S36440

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S78040

A;Molecule type: mRNA

A;Residues: 1-685 <PAN>

A;Cross-references: EMBL:X70854

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL Data Library, January 1993

A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement membrane ligands.

A;Reference number: S36440
 A;Accession: S78560
 A;Molecule type: mRNA
 A;Residues: 1-39, 'P', 41-685 <CHU>
 A;Cross-references: EMBL:X70854
 C;Genetics:
 A;Introns: 568/3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing; basement membrane; calcium binding;
 extracellular matrix; glycoprotein; plasma
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-685/Product: fibulin, splice form C #status predicted <MAT>
 F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 746; DB 2; Length 685;
 Best Local Similarity 36.3%; Pred. No. 1.3e-41;
 Matches 161; Conservative 64; Mismatches 153; Indels 66; Gaps 17;

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Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | |      : || :|| | | | :|| :| | | | | | | | |
Db      290 CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC----- 336

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | |      | | | : | : || || || ||
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAAPP 365

Qy      135 SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQQLCANVPGSYS 189
      : | | | | : | : | | | : | : | : | | | | | | | |
Db      366 AEPCGKGHHCLNSPGSFRCECKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFH 425

Qy      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEE-DGVHCSDM 248
      | : | : | | : | | | | : | | | | | : | | | | : | |
Db      426 CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      ||| :      : | : | | : : || | | | : | : | | : | |
Db      485 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC 544

Qy      306 YNLQGGFKCIDPIRCEEPYLRISDNRCM---CPAENPGCRDQPFTILYRDMDDVVSGRSVP 362
      : | : | | : | : | | | | : | | | | | | | | | : | |
Db      545 FNIQGSFRCLS-FECPENYRRSADTRCARLPC-HENQECPRPLRITYYHLSFPTNIQVP 602

Qy      363 ADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM 422
      | : | : | : | | | | : | | | | : | : | : | | : | : |
Db      603 AVVFRMGPPSSAVPGDSMQLAITAGNEEGFFTRKVVSHSGVVALTKPIPEPRDLLLTVKM 662

Qy      423 --ITVNTVINFRGSSVIRLRIYVS 444
      | | : | | : | | : | |
Db      663 DLYRHGTVSSF----VAKLFIFVS 682
  
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RESULT 4

C36346

fibulin 1 precursor, splice form C - human

N;Alternate names: fibulin C

N;Contains: fibulin 1 splice form A; fibulin 1 splice form C

C;Species: Homo sapiens (man)

C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 02-Aug-2002
 C;Accession: C36346; A36346; A32826
 R;Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
 J. Cell Biol. 111, 3155-3164, 1990
 A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.
 A;Reference number: A36346; MUID:91100426; PMID:2269669
 A;Accession: C36346
 A;Molecule type: mRNA
 A;Residues: 1-683 <ARG>
 A;Cross-references: GB:X53743; NID:g31418; PIDN:CAA37772.1; PID:g31419
 A;Accession: A36346
 A;Molecule type: mRNA
 A;Residues: 1-566 <AR2>
 A;Cross-references: GB:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415
 R;Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.
 Cell 58, 623-629, 1989
 A;Title: Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
 A;Reference number: A32826; MUID:89354537; PMID:2527614
 A;Accession: A32826
 A;Molecule type: protein
 A;Residues: 30-35, 'SX', 38-40, 'SH', 43-44 <AR3>
 C;Genetics:
 A;Gene: GDB:FBLN1; FBLN
 A;Cross-references: GDB:278285; OMIM:135820
 A;Map position: 22q13.3-22q13.3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing; glycoprotein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-683/Product: fibulin 1 splice form C #status predicted <MAT>
 F;180-214/Domain: EGF homology <EGF>
 F;485-523/Domain: EGF homology <EGF1>
 F;98,535,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.1%; Score 737; DB 2; Length 683;
 Best Local Similarity 35.4%; Pred. No. 4.9e-41;
 Matches 157; Conservative 67; Mismatches 154; Indels 66; Gaps 17;

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Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCPRTNPV 75
      | | : | | : | | | | : | | : | | | |
Db      288 CRP-----KLQCKSGFIQD-ALGNCIDINECLSIAPCPIGHTCINTEGSYTC----- 334

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | : | | : | | : | | : | | | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAFP 363

Qy      135 SHQCNPQTICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | : | | : | | : | | : | | : | |
Db      364 AEPCGKGHRCVNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYL 423

Qy      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
      | : | | | : | | | | : | | : | | : | | : | |
Db      424 CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 482

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      | | : : | : | | : | | : | | : | | : | |

```

Db 483 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC 542

Qy 306 YNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMVSVGRSVPA 363
 :|:| | |:| : | | | : | | | | | | : : | |

Db 543 FNIQGAFRCL-AFECPENYRRAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPA 601

Qy 364 DIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMI 423
 :|:| :| | | | | | | : | | : :|:|: | | : :

Db 602 VVFRMGPSAVPGDSMQLAITGGNEEGFPTTRKVSPPHSGVVALTKPVPEPRDL-----LL 656

Qy 424 TVNTVINFRG---SSVIRLRIYVS 444
 | | :| | | | | | | | | |

Db 657 TVKMDLSRHGTVSSSFVAKLFIFVS 680

RESULT 5

A49457

fibulin-2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-2002

C;Accession: A49457; S74095

R;Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.

J. Cell Biol. 123, 1269-1277, 1993

A;Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with multiple EGF-like repeats and consensus motifs for calcium binding.

A;Reference number: A49457; MUID:94064787; PMID:8245130

A;Accession: A49457

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1221 <PAN>

A;Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047

R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A;Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases and other tissue proteases.

A;Reference number: S74094; MUID:96439073; PMID:8841408

A;Accession: S74095

A;Molecule type: protein

A;Residues: 236-238,'X',240-247;260-275;336-344,'L',346-361;405-426;566-

568,'EM',569-589;653-666;784-787,'X',789-794;841-844,'X',846-850;883-

892,'X',894-894;930-935,'X',937-939 <SAS>

C;Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F;942-978/Domain: EGF homology <EGF>

Query Match 29.0%; Score 733.5; DB 2; Length 1221;

Best Local Similarity 35.3%; Pred. No. 1.4e-40;

Matches 146; Conservative 60; Mismatches 149; Indels 59; Gaps 11;

Qy 23 AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSN 82

|: |:| :| | | | | | | | | | | | | | | |

Db 829 ARQRCMDGF-LQDPEGNCVDINECTSLLEPCRSFGFSCINTVGSYTC----- 873

Qy 83 PYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPT 141

| |:| | | :| :| | | | | | | | |

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Db      874 -----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEG 909

Qy      142 QICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGF 196
      |:| | | | | | |:| |:|::|| || | | ||| |:| ||
Db      910 QLCYNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSAAGF 969

Qy      197 TLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSE 255
      | ||: |:|||| | | | | | |:| | | |:| || | |:|:| |:| :
Db      970 LLAADGKHCEDVNECETR- CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAG 1028

Qy      256 FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC 314
      || ||| |:| |:| || :: : |||:|::|| | |:| :|:|:| |:|
Db      1029 ILCTFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRC 1088

Qy      315 IDPIRCEEPLYLRISDNRCMCPAENPGCRD-----QPFTILYRMDVVSGRSVPADIFQM 368
      : | |:|:| :| | |:| | | : : :| ||| |:|:
Db      1089 L-RFDCPPNYVRVSQTKC----ERTTCQDITECQTS PARITHYQLNFQTGLLVP AHIFRI 1143

Qy      369 QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 422
      : | | || | |:| : : : |:| |:| |:|:|
Db      1144 GPAPAFAGDTISLTITKNGEEGYFVTRRLNAYTGVVSLORSVLEPRDEALDVEM 1197

```

C;Keywords: alternative splicing; extracellular matrix

F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-1184/Product: fibulin-2 protein #status predicted <MAT>
 F;905-941/Domain: EGF homology <EGF>

Query Match 28.0%; Score 709.5; DB 2; Length 1184;
 Best Local Similarity 34.3%; Pred. No. 5.1e-39;
 Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

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Qy      15 LCLPSPGN----AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIP 70
      || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      780 LCQNTKGSFYCQARQRCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC-- 836

Qy      71 RTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD 129
      ||||| || | : : ||||:
Db      837 -----QARNPLICARGYHASDDGAKCVDVN 860

Qy     130 ECATDSHQCNPTQICINTEGGYTCSTDGYW--LLEGQCLDIDECRYG---YCQQLCANV 184
      || | : | : | | | | | : | : : || | | |
Db     861 ECETGVHRCGEGQVCHNLPGSYRCDCCKAGFQDAFGRGCIDVNECWASPGRLCQHTCENT 920

Qy     185 PGSYSCTCNPGFILNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH 244
      ||| | : | || | || : ||||| : | | | | ||| : | | || : |||
Db     921 LGSYRCSCASGFLLAADGKRCEDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT 979

Qy     245 CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ 302
      | : : ||| : : | | | : | ||| : || | : : ||| : : || | : | :
Db     980 CTDIDECAQGAGILCTFRCLNVPGSYQCACPEQGYTMTANGRSCKDVEDCALGTHNCSEA 1039

Qy     303 QTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV 356
      : || : ||| | : | : | : : | : | | | | | : : :
Db    1040 ETCHNIQGSFRCL-RFECPPNYVQVSKTKC----ERTTCHDFLECQNSPARITHYQLNFQ 1094

Qy     357 SGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 416
      : | ||| || : : : | | | | | : : : : | : || :
Db    1095 TGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDF 1154

Qy      417 QLDLEM 422
      || : ||
Db    1155 ALDVEM 1160
  
```

RESULT 7

S34968

fibulin, splice form D precursor - mouse

N;Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002

C;Accession: S34968; S36441; S13814

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S34968

A;Molecule type: mRNA

A;Residues: 1-705 <PAN>

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its
calcium-dependent binding to other basement membrane ligands.
A;Reference number: S36440
A;Accession: S36441
A;Molecule type: mRNA
A;Residues: 1-39,'P',41-705 <PAW>
A;Cross-references: EMBL:X70854; NID:g396820; PIDN:CAA50207.1; PID:g396821
A;Experimental source: cell-line F9 teratocarcinoma
R;Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur. J. Biochem. 193, 651-659, 1990
A;Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90)
shared by basement membranes and serum.
A;Reference number: S13814; MUID:91065369; PMID:2249686
A;Accession: S13814
A;Molecule type: protein
A;Residues: 28;31-49,'X',51-53;'XX',110-117;231-240,'X',242-243;339-362,'S',364-
387;434-439;469-476;'Q',554-557,'Q',559-563;574-581 <KLU>
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; basement membrane; calcium binding;
extracellular matrix; glycoprotein; plasma
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-705/Product: fibulin, splice form D #status predicted <MAT>
F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.8%; Score 703.5; DB 2; Length 705;
Best Local Similarity 34.9%; Pred. No. 7.9e-39;
Matches 162; Conservative 67; Mismatches 156; Indels 79; Gaps 22;

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Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
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Db      290 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPVGGTCINTEGSYTC----- 336

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPP 365

Qy     135 SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     366 AEPCGKGHHCLNSPGSFRCEKAGFYFDGISRTCDINECQRYPGRLCGHKCENTPGSFH 425

Qy     190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     426 CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484

Qy     249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTC 305
      | | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db     485 DECALPTGGHICSYRCINIPGSFQCSPPSGYRLAPNGRNCQDIDECVTGIHNCSINETC 544

Qy     306 YNLQGGFKCIDPIRCEEPYLRI SDN-----RCM--CPAENPGC-RDQPFTILYRDM 353
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     545 FNIQGSFRCLS-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVI 603

Qy     354 DVVSGRSV--PADIFQMATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLV 405
      : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     604 SLPTFREFTRP EII FLRAVTPLYPANQADI IFDITEGNLRDSFDII KRYEDGMTVGVV 663

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Qy	16	CLPSPGNAQAQACTNGFQCLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV	75
Db	288	CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC-----	334
Qy	76	YRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD	134
Db	335	-----QKNVPN-----CGRGYHLNEEGTRCVDVDECAAPP	363
Qy	135	SHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS	189
Db	364	AEPCKGKHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL	423
Qy	190	CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEE-DGVHCSDM	248
Db	424	CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQYCRRGYQLSDVDGVTCEDI	482
Qy	249	DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC	305
Db	483	DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC	542
Qy	306	YNLQGGFKCIDPIRCEEPYLR	326
Db	543	FNIQGAFRCL-AFECPENYRR	562

RESULT 9

T42760

fibulin, splice form D precursor - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 23-Sep-2002

C;Accession: T42760

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and
characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42760

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-689 <BAR>

A;Cross-references: EMBL:AF051401; PIDN:AAC28321.1

C;Genetics:

A;Note: FBLN1

Query Match 23.9%; Score 606.5; DB 2; Length 689;
Best Local Similarity 27.3%; Pred. No. 1.7e-32;
Matches 159; Conservative 53; Mismatches 163; Indels 207; Gaps 20;

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Qy      15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTN 73
      || | : | : ||| | : |||| | : : | : | : ||
Db      167 LCHDRGGEKVECSRSGFDLAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI---- 222

Qy      74 PVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECA 132
      | | | | | | | : : | | | |
Db      223 -----RTLSCGTGYAMDSETERCRDVDECN 247

Qy      133 TDSHQCNPTQICINTEGGYTC-----SCTDGYWLLEGQCLDIDE 171
      || | | | | : | | | | : | : | | | |
Db      248 LGSHDCGPLYQCRNTQGSYRCDAKKCGDQELQNPMTGECTSITCPNGYYPKNGMCDNIDE 307

Qy      172 CRYGY-----CQQ---LCA-----N 183
      | | : | | | | |
Db      308 CVTGHNCGAGEECVNTPGSFRCQQKGNLCAHGYEVNGATGFCEQVNECQQGVCGSMECIN 367

Qy      184 VPGSYSCTCNPFTLNE----- 200
      : || : | | | | : | :
Db      368 LPGTYKCKCGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLA 427

Qy      201 -DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----S 254
      || | | : || | | | | | | | | | : | | | | : || | |
Db      428 SDGRRCEDVNECTTGIAACEQKCVNIPGSYQICDRGFALGPDGTKCEDIDECSIWAGSG 487

Qy      255 EFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC 314
      || | : | : | | | | | : | : | : | | : | | | |
Db      488 NDLCMGGCINTKGSYLQCQPPGYKIQPDGRTCDVDDECA-MGECAGSDKVCVNTLGSFKC 546

Qy      315 IDPIRCEEPYLRISDNR-----C--MCPAENPGC-RDQPFTILYRDMVDVSGRSV-- 361
      | | | : | | : | : | : | : | : | : | : | : |
Db      547 -HSIDCPTNYIHDSLKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIIIS 605

```

QY 362 PADI-----FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIK 411
 | :: | : | | : :: | | : : : ||
 Db 606 PIEVSRIVTHMGVPFSDYNDLYVGQRHFRIVQERNIG-----IVQLVKPIS 652

QY 412 GPREIQLDLEMITVNTVINFRGSSVIR-----LRIYVSQYPF 448
 || : | | | | : : : | | : |||
 Db 653 GP-----TVETIKVNIHTKSRTGVILAFNEAIEISVSKYPF 689

RESULT 10

T42990

fibulin 1, splice form C precursor - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T42990

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.

submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42990

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-712 <BAR>

A;Cross-references: EMBL:AF051402; PIDN:AAC28322.1

C;Genetics:

A;Gene: FBLN1

C;Superfamily: fibulin-1; EGF homology

C;Keywords: alternative splicing; basement membrane; extracellular matrix

Query Match 23.7%; Score 599.5; DB 2; Length 712;
 Best Local Similarity 27.8%; Pred. No. 5.1e-32;
 Matches 155; Conservative 47; Mismatches 153; Indels 203; Gaps 19;

QY 15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTN 73
 || | : | : ||| | : ||| | : | : | : ||
 Db 167 LCHDRGGEKVECSRSGLDAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI---- 222

QY 74 PVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDDECA 132
 | | | | | | : : | | |||
 Db 223 -----RTLSCGTGYAMDSETERCRDVDDECN 247

QY 133 TDSHCNPTQICINTEGGYTC-----SCTDGYWLLEGQCLDIDE 171
 || | | | || : | | | : | : || : | | |||
 Db 248 LGSHDCGPLYQCRNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCDIDE 307

QY 172 CRYGY-----CQQ---LCA-----N 183
 | | : ||| ||| |
 Db 308 CVTGHNCGAGEECVNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECIN 367

QY 184 VPGSYSCTCNPFGFTLNE----- 200
 : || : | | | | : :
 Db 368 LPPTYKCKCGPGYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLA 427

QY 201 -DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----S 254
 ||| | : ||| | | | | | : | | | : | | | : |||
 Db 428 SDGRRCEDVNECTTGIAACEQKCVNIPGSYQCICDRGFALGPDGKCEDIDECSIWAGSG 487

Qy 255 EFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKC 314
 || | : | : | | | | : | : | : | : | : | | | |
 Db 488 NDLCMGGCINTKGSYLCCQPPGYKIQPDGRTCDVDDECA-MGECAGSDKVCVNTLGSFKC 546

Qy 315 IDPIRCEEPYLRI SDNR-----CMCPAENPGCRDQPF TILYRDMDVVSGRSVP--- 362
 | | | : | : | | | | | : | : : | : | |
 Db 547 -HSIDCPTNYIHDSLKNRCNRQPSACGLPEE---CSKVPLFLTYQFISL--ARAVPISS 600

Qy 363 -----ADI---FQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISA 402
 | | | : | | | : | : | | | |
 Db 601 HRPAILTFKVSAPNHADTEVNFELQLKTTIVGAPNVLPAIRAN----FLLQKGEKRNSA 655

Qy 403 TLVMTRPIKGPREIQLDL 420
 : : : | : : | |
 Db 656 VVTLRDSL DGPQTVKLQL 673

RESULT 11

T43210

fibulin-1D precursor - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T43210

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
 submitted to the EMBL Data Library, June 1998

A;Description: Identification of chicken and *C. elegans* fibulin-1 homologs and
 characterization of the *C. elegans* fibulin-1 gene.

A;Reference number: Z22337

A;Accession: T43210

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-589 <BAR>

A;Cross-references: EMBL:AF070477; PIDN:AAC24035.1

C;Genetics:

A;Note: intron positions not resolved (incomplete sequence)

C;Superfamily: fibulin-1; EGF homology

Query Match 23.5%; Score 596; DB 2; Length 589;
 Best Local Similarity 27.3%; Pred. No. 7.4e-32;
 Matches 159; Conservative 53; Mismatches 163; Indels 208; Gaps 21;

Qy 15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLD-IDECRTIPEACRGDMMCVNQNGGYLCIPRT 72
 || | : | : || | | | : | | | | : : | : | | : ||
 Db 66 LCHDRGGEKVECSRS GFDLAPDGMACVDHIDECA TLMDDCLESQRCLNTPGSFKCI--- 122

Qy 73 NPVYRGYPYSPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCV DVDEC 131
 | | | | | | | : : | | | | |
 Db 123 -----RTLSCGTGYAMDSETERCRD VDEC 146

Qy 132 ATDSHQCNPTQICINTEGGYTC-----SCTDGYWLLEGQCLDID 170
 || | | | | | : | : | : | | | |
 Db 147 NLGSHDCGPLYQCRNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDID 206

Qy 171 ECRYGY-----CQQ---LCA----- 182
 || | : | | | | |
 Db 207 ECVTGHNCGAGEECVNTPGSFRCCQKGNLCAHGYEVNGATGFCE DVNECQQGVCGSMECI 266

Qy 183 NVPGSYSCTCNPGLTNE----- 200
 |::| | |:: |:
 Db 267 NLPPTYKCKCGPYEFNDAKKRCEVDCEIKFAGHVCDLSAECINTIGSFECKCKPGFQL 326

Qy 201 --DGRSCQDVNECATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF---- 253
 ||| |::||| | | | |:: | | | | | |::|||
 Db 327 ASDGRRCEDVNECTTGIAACEQKCVNI PGSYQCICDRGFALGPDGTKCEDIDECSTWAGS 386

Qy 254 SEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFK 313
 || |:: |:: | | | |:: | | | |:: | | | |
 Db 387 GNDLCMGGCINTKGSYLCQCPPGYKIQPDGRTCDVDDECA-MGECAGSDKVCVNTLGSFK 445

Qy 314 CIDPIRCEEPYLRISDNR-----C--MCPAENPGC-RDQPFITLYRDMVVSGRSV- 361
 | | | |:: | | | |:: | | | |:: | | | |::
 Db 446 C-HSIDCPTNYIHDSLKNQIADGYSCI KVCSTEDTECLGNHTREVLYQFRAVPSLKTII 504

Qy 362 -PADI-----FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPI 410
 |:: | | | |:: | | | |:: | | | |:: | | | |
 Db 505 SPIEVSRIVTHMGVPPFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPI 551

Qy 411 KGPREIQLDLEMITVNTVINFRGSSVIR-----LRIYVSQYPF 448
 || |:: | | | |:: | | | |:: | | | |
 Db 552 SGP-----TVETIKVNIHTKSRTGVILAFNEAIIISVSKYPF 589

RESULT 12

T22793

hypothetical protein F56H11.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002

C;Accession: T22793; T24489

R;Wilkinson, J.

submitted to the EMBL Data Library, January 1996

A;Reference number: Z19616

A;Accession: T22793

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WIL>

A;Cross-references: EMBL:Z68749; PIDN:CAA92962.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone F56H11

R;Lloyd, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19897

A;Accession: T24489

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WI2>

A;Cross-references: EMBL:Z68219; PIDN:CAA92483.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone T05A1

C;Genetics:

A;Gene: CESP:F56H11.1

A;Map position: 4

A;Introns: 14/1; 92/3; 144/1; 195/1; 281/1; 325/2; 371/2; 390/1; 437/1; 471/3;
 498/3; 607/1; 649/2; 718/1

C;Superfamily: fibulin-1; EGF homology

Query Match 22.8%; Score 577.5; DB 2; Length 798;
 Best Local Similarity 26.7%; Pred. No. 1.6e-30;
 Matches 162; Conservative 50; Mismatches 180; Indels 215; Gaps 23;

```

Qy      15 LCLPSPG-NAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLC----- 68
      || | : | :||| | :| :|| | | || | |||:|
Db      167 LCHDRGGEKVECSRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRIS 226

Qy      69 --IP---RTNPVYRGP---YSNPYSTPYSGPYAAAPP----- 98
      :| | | : | :||| :| | | :
Db      227 RLVPHRHRANRIGNAPRRMRDDPYSR--AGEYREASQANTEFGCPMGWLFQHGHCVDIDE 284

Qy      99 -----LSAPNYPTISRPLICRFGYQMD---ESNQC----- 126
      | : | | | | | | | | | | | |
Db      285 CATLMDDCLESQRCLNTPGSFKCIRTLSCTGYAMDSETERNNCFIILNNTFNCKYFFV 344

Qy      127 -DVDECATDSHQCNPTQICINTEGGYTCS----- 154
      ||||| || | | |||:| | |
Db      345 EDVDECNLGSHDCGPLYQCRNTQGSYRCDAKKCGDGELQNPMTGEYIDECVTGHNCGAGE 404

Qy      155 -----CTDGYWL--LEGQCLDIDECRYGYCQQL-CANVPGSYSCTCNP 194
      | || : | | :||| | | : | | :||| | | |
Db      405 ECVNTPGSFRCQQKGNLCAHGYEVNGATGFCEDEVNECQQGVCGSMECINLPGTYKCKCGP 464

Qy      195 GFTLNE-----DGRSCQDVNE 210
      |: |: ||| |:|||
Db      465 GYEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNE 524

Qy      211 CATE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSF---SEFLCQHECVNQ 265
      | | | | ||| ||: | | | : | | | | :||| | | | :|
Db      525 CTTGIAACEQKCVNIPGSYQICDRGFALGPDGTKCEDIDECISIWAGSGNDLCMGGCINT 584

Qy      266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 325
      |:| | ||||| : | |:| |:| | : | | | ||| | | | :
Db      585 KGSYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYI 642

Qy      326 RISDN-----CMCPAENPGCRDQPFTILYRDMDVVSGRSVP----- 362
      | |: | | | | | | | | : : : | :||
Db      643 HDSLKNKRCNRQPSACGLPEE---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVS 697

Qy      363 ----ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGP 413
      || | :| | | | : | :| | | | : : : | |
Db      698 APNHADTEVNFELQLKTTIVGAPNVLPAIRAN-----FLLQKGEKRNSAVVTLRDSL DGP 752

Qy      414 REIQLDL 420
      : :| |
Db      753 QTVKLQL 759
  
```

RESULT 13

A35626

transforming growth factor beta-1-binding protein - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 11-Jan-2000

C;Accession: A35626

R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claesson-Welsh, L.; Heldin, C.H.

Cell 61, 1051-1061, 1990

A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1 with multiple repeat sequences.

A;Reference number: A35626; MUID:90275601; PMID:2350783

A;Accession: A35626

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1394 <KAN>

A;Cross-references: GB:M34057; NID:g339547; PIDN:AAA61160.1; PID:g339548

C;Superfamily: unassigned EGF-related proteins; EGF homology

C;Keywords: alternative splicing

F;750-791/Domain: EGF homology <EGF>

Query Match 21.5%; Score 544; DB 2; Length 1394;
Best Local Similarity 29.4%; Pred. No. 4e-28;
Matches 128; Conservative 52; Mismatches 134; Indels 122; Gaps 17;

```
QY      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      562 CINLPVRYTCICYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSFLCI----- 614

QY      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLI-----CRFGYQ 118
      : | : : : | | : | : | | | | | | | | | | | | | | | | |
Db      615 -----CPAGFMASEEGTNCIDVDECLRPDVCGEHCVNTVGAFRCEYCDSGYR 662

QY     119 MDESNCVDVDECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGY 176
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     663 MTQRGRCEDIDDECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLPNV 720

QY     177 CQQ-LCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- 219
      | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db     721 CANGDCSNLEGSYMC SCHKG YTRTPDHKHC RDIDECQQGNLCVNGQCKNTEGSFRCTCGQ 780

QY     220 -----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF 253
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     781 GYQLSAAKDQCEDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCE DINECLE 840

QY     254 SEFLCQH-ECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGF 312
      : : | | : | : | | | | | | | | | | | | | | | | | | | | |
Db     841 DKSVCQRGDCINTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSF 898

QY     313 KCI-----DPIRCEEPYLRIS-----DN-----RCMC-----PAENPGCR 342
      | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     899 HCVCQQGFSISADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCLCYQGFQAPQDGQGCV 958

QY     343 DQPFTILYRDMDVVSG 358
      | : : : | |
Db     959 D-----VNECELLSG 968
```

RESULT 14

A47221

fibrillin 1 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end.

A;Reference number: A47221; MUID:94010947; PMID:7691719

A;Accession: A47221

A;Molecule type: mRNA

A;Residues: 1-337,'T',339-1029 <COR>

A;Cross-references: GB:X63556

R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bonadio, J.

Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene product in Marfan syndrome.

A;Reference number: I54355; MUID:93372860; PMID:8364578

A;Accession: I54355

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 132-3002 <PER>

A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; PID:g306746

R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.

Nature 352, 334-337, 1991

A;Title: Partial sequence of a candidate gene for the Marfan syndrome.

A;Reference number: S17064; MUID:91304568; PMID:1852207

A;Accession: S17064

A;Molecule type: mRNA

A;Residues: 1030-3002 <MAS>

A;Cross-references: EMBL:X63556

R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.

Science 259, 680-683, 1993

A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.

A;Reference number: I59574; MUID:93157831; PMID:8430317

A;Accession: I59574

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 2217-2288,'I',2290-2325 <RES>

A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861

R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.;

Tsipouras, P.; Ramirez, F.; Hollister, D.W.

Nature 352, 330-334, 1991

A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.

A;Reference number: S17062; MUID:91304567; PMID:1852206

A;Accession: S17062

A;Molecule type: mRNA

A;Residues: 'VLVTVVFIFLSYNKML',944-1444 <LEE1>

A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015

A;Accession: S62111

A;Molecule type: protein

A;Residues: 1166-1176,'X',1178-1180,'D',1182-1185 <LEE2>

R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.

J. Biol. Chem. 264, 21381-21385, 1989

A;Title: Connective tissue microfibrils. Isolation and characterization of three large pepsin-resistant domains of fibrillin.

A;Reference number: A34198; MUID:90078246; PMID:2512293

A;Accession: A34198

A;Molecule type: protein

A;Residues: 565-575;1890-1892,'I',1894-1900 <MAD>
 C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C;Genetics:
 A;Gene: GDB:FBN1
 A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A;Map position: 15q21.1-15q21.1
 A;Introns: 2236/1; 2258/1; 2297/1
 C;Superfamily: fibrillin 1; EGF homology
 C;Keywords: alternative splicing; calcium binding; extracellular matrix;
 glycoprotein; Marfan syndrome
 F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status
 predicted <MATA>
 F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted
 <MATC>
 F;1332-1367/Domain: EGF homology <EGF>
 F;1457-1492/Domain: EGF homology <EGF2>
 F;2262-2295/Domain: EGF homology <EGF1>

Query Match 21.0%; Score 532.5; DB 2; Length 3002;
 Best Local Similarity 30.1%; Pred. No. 4.5e-27;
 Matches 124; Conservative 50; Mismatches 125; Indels 113; Gaps 18;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDI DECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | : | : : | : || | | : | | | | | | : | | | | | : | :
Db      1175 CRNTIGSFKCRCDSGFALDSEERNCTDI DECRI SPDL C-GRGQCVNTPGDFEC--KCDEG 1231

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISR----PLICRF----- 115
      | : : : : : : : | | | | | | | | : | | | | | : | :
Db      1232 YESGF-----MMMKNCMDI DECQRDPLLCRGGVCHNTEGSYRCECPP 1273

Qy      116 GYQMD E S-NQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDI DEC 172
      | : | : : : | : | : | | : | | | | | : | | | | | : | :
Db      1274 GHQLSPNISACIDINECELSAHL C-PNGRCVNLI GKYQCACNFGYHSTPDRLFCVDI DEC 1332

Qy      173 RY--GYCQQLCANVPGSYSCTCNP GFTLNEDGRSCQDVNECATENP----- 216
      | | : | | | | | | : | | | | | | | | | | : | | : | |
Db      1333 SIMNGGCETFC TNSEGSYECSCQPGFALMPDQRSCDI DEC-EDNPNICDGGQCTNIPGE 1391

Qy      217 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHC 245
      | | | | | | | | | | | | | | | | | | | | : | | |
Db      1392 YRCLCYDGFMA SEDMKTCVDVNECDLNPNI CLSGTCENTKGSFICHCDMGYSGKKGTGC 1451

Qy      246 SDMDECSFSEFLC-QHE-CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQ 303
      : | : | | | : | | | | : : | | | | : | | | : | : | :
Db      1452 TDINECEIGA HNC GKHAVCTNTAGSFKCS CSPGWI--GDGIKCTDLDECSNGTHMCSQHA 1509

Qy      304 TCYNLQGGFKCIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 345
      | | | : : | : | | | | | | : | : | | | : |
Db      1510 DCKNTMGSYRCL---CKEGYTG DGFTCTDLDECS ENLNL C--GNGQCLNAP 1555

```

RESULT 15

A55567

fibrillin I - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002

C;Accession: A55567

R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.
 Genomics 23, 480-485, 1994
 A;Title: Sequence of the coding region of the bovine fibrillin cDNA and
 localization to bovine chromosome 10.
 A;Reference number: A55567; MUID:95137597; PMID:7835900
 A;Accession: A55567
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2871 <TIL>
 A;Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428
 C;Superfamily: fibrillin 1; EGF homology
 F;1201-1236/Domain: EGF homology <EGF>

Query Match 21.0%; Score 531.5; DB 2; Length 2871;
 Best Local Similarity 29.6%; Pred. No. 5e-27;
 Matches 122; Conservative 48; Mismatches 129; Indels 113; Gaps 16;

```

Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | : | : : | : || || : | ||||| | : | | ||| | : | : :
Db      1044 CRNTIGSFKRCRCDSGFALDSEERNCTDIDECRISPDLG-GRGQCVNTPGDFEC--KCDEG 1100

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISR----PLICRFGYQMDSE----- 122
      | : : : : : : | | | | | : | : :
Db      1101 YESGF-----MMMKNCMDIDECQRDPLLCRGGVCLNTEGSYRCECPP 1142

Qy      123 -----NQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDEC 172
      : | : | : | : | | | | : | | | | : | | : | : | : | :
Db      1143 GHQLAPNISACIDINECELSAHLG-PHGRVCNLIKGYQCACNPGYHSTPDRLFCVDIDEC 1201

Qy      173 RY--GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 216
      | | : | | ||| | : | ||| | | ||| | : | | : | |
Db      1202 SIMNGGCETFTCTNSEGSYECSCQPGFALMPDQRSCTDIDEC-EDNPNICDGGQCTNIPGE 1260

Qy      217 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHC 245
      || || || || || || || || || : : |
Db      1261 YRCLCYDGFMASEDMKTCVDVNECDLNPNI CLSGTCENTKGSFICHCDMGYSGKKGKTGC 1320

Qy      246 SDMDECSFSEFLCQHE--CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQ 303
      : | : | | | | | | : | : | | | : | | | : | : | : | :
Db      1321 TDINECEIGAHNCDRHAVCTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHA 1378

Qy      304 TCYNLQGGFKCIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 345
      | | | : : | : | | | | : | : | | | : | : |
Db      1379 DCKNTMGSYRCL---CKEGYTGDGFTCTDLDECSNENLNLG--GNGQCLNAP 1424

```

Search completed: January 9, 2004, 12:34:53
 Job time : 19.9736 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 10.287 Seconds
(without alignments)
2048.013 Million cell updates/sec

Title: US-09-674-379A-13
Perfect score: 2533
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2533	100.0	448	1	FBL5_HUMAN	Q9ubx5 homo sapien
2	2406	95.0	448	1	FBL5_RAT	Q9wvh8 rattus norv
3	2405	94.9	448	1	FBL5_MOUSE	Q9wvh9 mus musculu
4	1290	50.9	443	1	FBL4_CRIGR	O55058 cricetulus
5	1289	50.9	443	1	FBL4_HUMAN	O95967 homo sapien
6	1282	50.6	443	1	FBL4_MOUSE	Q9wvj9 mus musculu
7	1109.5	43.8	493	1	FBL3_RAT	O35568 rattus norv
8	1101	43.5	493	1	FBL3_HUMAN	Q12805 homo sapien
9	733.5	29.0	1221	1	FBL2_MOUSE	P37889 mus musculu
10	728	28.7	598	1	FBL1_CERAE	Q8mjj9 cercopithec
11	722	28.5	704	1	FBL1_CHICK	O73775 gallus gall
12	709.5	28.0	1184	1	FBL2_HUMAN	P98095 homo sapien
13	701.5	27.7	703	1	FBL1_HUMAN	P23142 homo sapien
14	700.5	27.7	705	1	FBL1_MOUSE	Q08879 mus musculu
15	631	24.9	681	1	FBL1_BRARE	O42182 brachydanio
16	577.5	22.8	798	1	FBL1_CAEEL	O77469 caenorhabdi
17	544	21.5	1394	1	LTBS_HUMAN	P22064 homo sapien

18	544	21.5	1595	1	LTBL_HUMAN	Q14766	homo sapien
19	532.5	21.0	2871	1	FBN1_HUMAN	P35555	homo sapien
20	531.5	21.0	2871	1	FBN1_BOVIN	P98133	bos taurus
21	525.5	20.7	2871	1	FBN1_PIG	Q9tv36	sus scrofa
22	523	20.6	1712	1	LTBL_RAT	Q00918	rattus norv
23	521	20.6	1389	1	LTBS_MOUSE	Q8cg18	mus musculu
24	521	20.6	1713	1	LTBL_MOUSE	Q8cg19	mus musculu
25	518.5	20.5	2871	1	FBN1_MOUSE	Q61554	mus musculu
26	518.5	20.5	2907	1	FBN2_MOUSE	Q61555	mus musculu
27	517.5	20.4	2911	1	FBN2_HUMAN	P35556	homo sapien
28	475	18.8	956	1	MTN2_HUMAN	O00339	homo sapien
29	452	17.8	956	1	MTN2_MOUSE	O08746	mus musculu
30	421	16.6	931	1	EMR1_MOUSE	Q61549	mus musculu
31	392	15.5	886	1	EMR1_HUMAN	Q14246	homo sapien
32	379	15.0	2470	1	NTC2_MOUSE	O35516	mus musculu
33	377	14.9	2471	1	NTC2_HUMAN	Q04721	homo sapien
34	375	14.8	810	1	NEL1_HUMAN	Q92832	homo sapien
35	372.5	14.7	816	1	NEL2_MOUSE	Q61220	mus musculu
36	371.5	14.7	2471	1	NTC2_RAT	Q9qw30	rattus norv
37	366	14.4	816	1	NEL2_HUMAN	Q99435	homo sapien
38	364	14.4	810	1	NEL1_RAT	Q62919	rattus norv
39	360.5	14.2	816	1	NEL_CHICK	Q90827	gallus gall
40	359.5	14.2	1964	1	NTC4_MOUSE	P31695	mus musculu
41	359	14.2	816	1	NEL2_RAT	Q62918	rattus norv
42	356	14.1	2703	1	NOTC_DROME	P07207	drosophila
43	355.5	14.0	2437	1	NTC1_BRARE	P46530	brachydanio
44	350.5	13.8	652	1	CD93_HUMAN	Q9np3	homo sapien
45	347.5	13.7	2556	1	NTC1_HUMAN	P46531	homo sapien

ALIGNMENTS

RESULT 1

FBL5_HUMAN

ID FBL5_HUMAN STANDARD; PRT; 448 AA.
AC Q9UBX5; O75966;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Urine p50 protein) (UP50).
GN FBLN5 OR DANCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Kostka G.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,

RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
 RT "DANCE, a novel secreted RGD protein expressed in developing,
 RT atherosclerotic, and balloon-injured arteries.";
 RL J. Biol. Chem. 274:22476-22483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urine;
 RA Zemel R., Sholto O., Shaul Y.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
 CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
 CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
 CC DEVELOPMENT AND REMODELING.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART, OVARY, AND
 CC COLON BUT ALSO IN KIDNEY, PANCREAS, TESTIS, LUNG, AND PLACENTA.
 CC NOT DETECTABLE IN BRAIN, LIVER, THYMUS, PROSTATE, OR PERIPHERAL
 CC BLOOD LEUKOCYTES.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; AJ133490; CAB38568.1; -.
 DR EMBL; AF112152; AAD41768.1; -.
 DR EMBL; AF093118; AAC62107.1; -.
 DR HSSP; P00736; 1APQ.
 DR Genew; HGNC:3602; FBLN5.
 DR MIM; 604580; -.
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005178; F:integrin binding activity; TAS.
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	288	333	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	SITE	54	56	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	131	144	BY SIMILARITY.
FT	DISULFID	138	153	BY SIMILARITY.
FT	DISULFID	155	166	BY SIMILARITY.
FT	DISULFID	172	181	BY SIMILARITY.
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	192	205	BY SIMILARITY.
FT	DISULFID	211	221	BY SIMILARITY.
FT	DISULFID	217	230	BY SIMILARITY.
FT	DISULFID	232	245	BY SIMILARITY.
FT	DISULFID	251	262	BY SIMILARITY.
FT	DISULFID	258	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	305	BY SIMILARITY.
FT	DISULFID	299	314	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	CARBOHYD	283	283	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	69	70	IP -> HS (IN REF. 3).
FT	CONFLICT	147	148	TE -> MK (IN REF. 3).
SQ	SEQUENCE	448 AA;	50180 MW;	19FCA51FDA328003 CRC64;

Query Match 100.0%; Score 2533; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.4e-180;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Db	1	MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
Qy	61	NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD	120
Db	61	NQNGGYLCIPRTNPVYRGYPYSPYSGYPAAAPPLSAPNYPTISRPLICRFGYQMD	120
Qy	121	ESNQCDVDDECATDSHCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECYGYCQQL	180
Db	121	ESNQCDVDDECATDSHCNPTQICINTEGGYTCSTDGYWLLEGQCLDIDECYGYCQQL	180
Qy	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Db	181	CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE	240
Qy	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Db	241	DGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCN	300
Qy	301	LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS	360
Db	301	LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMPAENPGCRDQPFTILYRDMDVVSGRS	360
Qy	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL	420
Db	361	VPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL	420
Qy	421	EMITVNTVINFRGSSVIRLRIYVSQYPF	448

Db

421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

RESULT 2

FBL5_RAT

ID FBL5_RAT STANDARD; PRT; 448 AA.
AC Q9WVH8; Q9R284;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
DE protein) (EVEC).
GN FBLN5 OR DANCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99278197; PubMed=10347091;
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein
RT upregulated in embryonic and diseased adult vasculature.";
RL Circ. Res. 84:1166-1176(1999).
CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC DEVELOPMENT AND REMODELING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC -----
DR EMBL; AF112153; AAD41769.1; -.
DR EMBL; AF137350; AAD25101.1; -.
DR HSSP; P00736; 1APQ.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.


```

Db      241 DGIHCSDMDECSFSEFLCQHECVNQPGSYFCSCPPGYVLLEDNRSCQDINECEHRNHTCT 300
QY      301 LQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRS 360
Db      301 PLQTCYNLQGGFKCIDPIVCEEPYLLIGDNRCMCPAENTGCRDQPFTILFRMDMDVVSGRS 360
QY      361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
Db      361 VPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDL 420
QY      421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448
Db      421 EMITVNTVINFRGSSVIRLRIYVSQYPF 448

```

RESULT 3

FBL5_MOUSE

```

ID      FBL5_MOUSE      STANDARD;      PRT;      448 AA.
AC      Q9WVH9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE      EGF-like protein) (Dance).
GN      FBLN5 OR DANCE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99357779; PubMed=10428823;
RA      Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA      Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA      Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT      "DANCE, a novel secreted RGD protein expressed in developing,
RT      atherosclerotic, and balloon-injured arteries.";
RL      J. Biol. Chem. 274:22476-22483(1999).
CC      -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC      INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC      LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC      DEVELOPMENT AND REMODELING.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 6 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF112151; AAD41767.1; -.
DR      HSSP; P00736; 1APQ.

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DR   MGD; MGI:1346091; Fbln5.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   Pfam; PF00008; EGF; 4.
DR   SMART; SM00179; EGF_CA; 4.
DR   PROSITE; PS00010; ASX_HYDROXYL; 4.
DR   PROSITE; PS00022; EGF_1; FALSE_NEG.
DR   PROSITE; PS01186; EGF_2; 4.
DR   PROSITE; PS01187; EGF_CA; 6.
KW   Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
KW   Glycoprotein.
FT   SIGNAL          1      23      POTENTIAL.
FT   CHAIN           24     448     FIBULIN-5.
FT   DOMAIN          24      69     EGF-LIKE 1, DIVERGENT.
FT   DOMAIN          127     167     EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN          168     206     EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN          207     246     EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN          247     287     EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT   DOMAIN          288     333     EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT   SITE            54      56     CELL ATTACHMENT SITE (POTENTIAL).
FT   DISULFID        131     144     BY SIMILARITY.
FT   DISULFID        138     153     BY SIMILARITY.
FT   DISULFID        155     166     BY SIMILARITY.
FT   DISULFID        172     181     BY SIMILARITY.
FT   DISULFID        177     190     BY SIMILARITY.
FT   DISULFID        192     205     BY SIMILARITY.
FT   DISULFID        211     221     BY SIMILARITY.
FT   DISULFID        217     230     BY SIMILARITY.
FT   DISULFID        232     245     BY SIMILARITY.
FT   DISULFID        251     262     BY SIMILARITY.
FT   DISULFID        258     271     BY SIMILARITY.
FT   DISULFID        273     286     BY SIMILARITY.
FT   DISULFID        292     305     BY SIMILARITY.
FT   DISULFID        299     314     BY SIMILARITY.
FT   DISULFID        320     332     BY SIMILARITY.
FT   CARBOHYD        283     283     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD        296     296     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE        448 AA;  50193 MW;  F15CC70CCFBFDC97 CRC64;

```

[illegible]

DR InterPro; IPR001491; ThrmBomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 127 140 BY SIMILARITY.
 FT DISULFID 134 149 BY SIMILARITY.
 FT DISULFID 151 162 BY SIMILARITY.
 FT DISULFID 168 177 BY SIMILARITY.
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 188 201 BY SIMILARITY.
 FT DISULFID 207 217 BY SIMILARITY.
 FT DISULFID 213 226 BY SIMILARITY.
 FT DISULFID 228 241 BY SIMILARITY.
 FT DISULFID 247 258 BY SIMILARITY.
 FT DISULFID 254 267 BY SIMILARITY.
 FT DISULFID 269 281 BY SIMILARITY.
 FT DISULFID 287 300 BY SIMILARITY.
 FT DISULFID 294 309 BY SIMILARITY.
 FT DISULFID 315 327 BY SIMILARITY.
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 443 AA; 49432 MW; 0BCFE5D7323D9E5F CRC64;

Query Match 50.9%; Score 1290; DB 1; Length 443;
 Best Local Similarity 50.1%; Pred. No. 1.5e-88;
 Matches 227; Conservative 71; Mismatches 133; Indels 22; Gaps 5;

QY 1 MPGIKRILTVTILALCLPSGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
 :|| : : :| | || :: :||:|:| | | | :|| |||||:|
 Db 8 LPGSLLLWALLLLLLLGAASPQDSEEPDSYTECTDGYEWDADSQHCRDVNECLTIPEACKG 67

 QY 56 DMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRF 115
 :| |:| |||||:|:| : : || | || | |
 Db 68 EMKCINHYGGYLCIPRSAAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP 111

 QY 116 GYQMDESNCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYG 175
 ||: || ||||| || | | :| | | | :| ||| : :|:|||||
 Db 112 GYEPDEQESCVDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKVGPECVDIDECRYR 171

 QY 176 YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
 ||| | |:|:|:| | ||| | : ||| ||||| || | |:|:|:|:|:|
 Db 172 YCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCNQG 231

QY 236 YELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
 ||| || |||:||||:| :|||: |||:| | : | || || || | |||:|||
 Db 232 YELHRDGFSCSDIDECSYSSYLQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECETG 290

QY 296 NHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDV 355
 | |: ||| | ||::|:| || |||::| ||| || ||:| |:|:| | :
 Db 291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYVQVSDNRCFCPVSNPLCREQPSSIVHRYMSI 350

QY 356 VSGRSPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTTRPIKGP 415
 | |||||:| |:| |: |||| | ||::| | :| |:| | :| | |: | |: |||
 Db 351 TSERSVPADVFIQATSVYPGAYNAFQIRAGNTQGDFYIRQINNVSAMLVLARPVTPG 410

QY 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||:|:|:::| |||:| |::| | |
 Db 411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443

RESULT 5

FBL4_HUMAN

ID FBL4_HUMAN STANDARD; PRT; 443 AA.
 AC O95967; O75967;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
 DE (Fibulin-4) (FIBL-4) (UPH1 protein).
 GN EFEMP2 OR FBLN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=20068041; PubMed=10601734;
 RA Giltay R., Timpl R., Kostka G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
 RL Matrix Biol. 18:469-480(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zemel R., Shaul Y.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435063; PubMed=10982184;
 RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;
 RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
 RT from the multiple retinopathy critical region on 11q13.";
 RL Hum. Genet. 106:66-72(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ132819; CAA10791.2; -.
 DR EMBL; AF093119; AAC62108.1; -.
 DR EMBL; AF109121; AAF65188.1; -.
 DR EMBL; BC010456; AAH10456.1; -.
 DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:3219; EFEMP2.
 DR MIM; 604633; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

Db 351 TSERSVPADV FQIQATSVYPGAYNAFQIRAGNSQGD FYIRQINNVSAMLV LARPVTGP RE 410

QY 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 |||||:|:|:::| |||:| |::| |

Db 411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443

RESULT 6

FBL4_MOUSE

ID FBL4_MOUSE STANDARD; PRT; 443 AA.

AC Q9WVJ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE EGF-containing fibulin-like extracellular matrix protein 2 precursor

DE (Fibulin-4) (FIBL-4) (Mutant p53 binding protein 1).

GN EFEMP2 OR FBLN4 OR MBP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RX MEDLINE=99308589; PubMed=10380882;

RA Gallagher W.M., Argentini M., Sierra V., Bracco L., Debussche L.,

RA Conseiller E.;

RT "MBP1: a novel mutant p53-specific protein partner with oncogenic

RT properties.";

RL Oncogene 18:3608-3616(1999).

CC -!- SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF104223; AAD45219.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:1891209; Efemp2.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR001491; Thrbomoduln.

DR Pfam; PF00008; EGF; 4.

DR PRINTS; PR00907; THRMBOMODULN.

DR SMART; SM00179; EGF_CA; 4.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF_2; 4.

DR PROSITE; PS01187; EGF_CA; 6.

KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 127 140 BY SIMILARITY.
 FT DISULFID 134 149 BY SIMILARITY.
 FT DISULFID 151 162 BY SIMILARITY.
 FT DISULFID 168 177 BY SIMILARITY.
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 188 201 BY SIMILARITY.
 FT DISULFID 207 217 BY SIMILARITY.
 FT DISULFID 213 226 BY SIMILARITY.
 FT DISULFID 228 241 BY SIMILARITY.
 FT DISULFID 247 258 BY SIMILARITY.
 FT DISULFID 254 267 BY SIMILARITY.
 FT DISULFID 269 281 BY SIMILARITY.
 FT DISULFID 287 300 BY SIMILARITY.
 FT DISULFID 294 309 BY SIMILARITY.
 FT DISULFID 315 327 BY SIMILARITY.
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 443 AA; 49425 MW; 4969C0328A23DD88 CRC64;

Query Match 50.6%; Score 1282; DB 1; Length 443;
 Best Local Similarity 49.9%; Pred. No. 5.7e-88;
 Matches 226; Conservative 70; Mismatches 135; Indels 22; Gaps 4;

QY 1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
 :|| : :| | || : : :||:|:| | | | :|| |||||:|
 Db 8 LPGSLLLWAFLLLLLGAASPDPEEPSYTECTDGYEWDADSQHCRDVNECLTIPEACKG 67
 QY 56 DMMCYNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRF 115
 :| |:| |||||:|:| | : : || | || :| |
 Db 68 EMKCINHYGGYLCIPRSAAVISDLHG-----EGPPPPAA-----HAQQPNPCPQ 111
 QY 116 GYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYG 175
 ||: || ||||| | | |:| | | | |:| ||| : :|:| |||||
 Db 112 GYEPDEQESCVDVDECTQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171
 QY 176 YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
 ||| | |:| |:| | | | | : ||| ||||| || | | |:| |:| |:| :|
 Db 172 YCQHRCVNLPGSFRQCCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCNQG 231
 QY 236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
 ||| || |||:| |:| :| |:| :| |:| :| | | || | | |||:|
 Db 232 YELHRDGFSCSDIDEQYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECETG 290
 QY 296 NHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDV 355
 | |: ||| | |:| |:| || |:| |:| |:| |:| || |:| |:| |:| :|
 Db 291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYVQVSDNRCLCPASNPLCREQPSSIVHRYMSI 350

FT	SIGNAL	1	17	POTENTIAL.
FT	CHAIN	18	493	EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT				MATRIX PROTEIN 1.
FT	DOMAIN	26	71	EGF-LIKE 1, DIVERGENT.
FT	DOMAIN	173	213	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	214	253	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	254	293	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	294	333	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	334	378	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	184	199	BY SIMILARITY.
FT	DISULFID	201	212	BY SIMILARITY.
FT	DISULFID	218	228	BY SIMILARITY.
FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
SQ	SEQUENCE	493 AA;	54596 MW;	22DAFD70BACF1CA5 CRC64;

Query Match 43.8%; Score 1109.5; DB 1; Length 493;
 Best Local Similarity 42.3%; Pred. No. 3.8e-75;
 Matches 206; Conservative 73; Mismatches 161; Indels 47; Gaps 5;

Qy	7	ILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGY	66
		: : :: : : :: : : :	
Db	9	MLTLALVKSQVTEETITYTQCTDGYEWDVPRQQCKDIDECDIVPDACKGGMKCVNHYGGY	68
Qy	67	LCIPRTNPVYRGPYSNPYSTPYS-----GPYPAAAPPLSAP	102
		: : : : : : : :	
Db	69	LCLPKTAQIIVNNEQPQQETPAAEASSGAATGTIAARSMATSGVIPGGGFIA SATAVAGP	128
Qy	103	NYPT-----ISRPLICRFGYQMDENQCVDVDECATDSHCNPTQ	142
		: : : :	
Db	129	EVQTGRNNFVIRRN PADPQRI PSNPSHRIQCAAGYEQSEHNV CQDIDECTSGTHNCRLDQ	188
Qy	143	ICINTEGGYTC SCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSY SCTCNPGFTLNED	201
		: : : : :	
Db	189	VCINLRGSFTCHCLPGYQKRGEQCVDIDEC SVPPYCHQGC VNTPGSFYCQCNPGFQLAAN	248
Qy	202	GRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCS DMDECSFSEFLCQHE	261
		: : : : : : : ::	
Db	249	NYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYL CQYQ	308
Qy	262	CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCE	321
		: : :: : : : : : :	
Db	309	CVNEPGKFSCMCPQGYQVV-RSRTCQDINECETTNE-CREDEM CWNYHGGFRCPQNPCQ	366
Qy	322	EPYLRI SDNR CMCPAENPGCRDQPFTILYRDM DVVSGRSVPADIFQM QATTRYPGAYYIF	381
		: : : : : : : : : :	
Db	367	DPYVLTS ENRCVCPVSN TMCRDVPQSI VYKYMNI RSDRSVPSDIFQIQATTIYANTINTF	426

QY 382 QIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI 441
 :||||| :||:| | :|| : : : ||| : |||:|:|:| :| :||:| |
 Db 427 RIKSGNENGFEYLRTSPVSAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLTI 486
 QY 442 YVSQYPF 448
 : : |
 Db 487 IVGPFSF 493

RESULT 8

FBL3_HUMAN

ID FBL3_HUMAN STANDARD; PRT; 493 AA.
 AC Q12805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 1 precursor
 DE (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein
 DE S1-5).
 GN EFEMP1 OR FBLN3 OR FBNL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND POSSIBLE ALTERNATIVE SPLICING.
 RC TISSUE=Skin;
 RX MEDLINE=95097983; PubMed=7799918;
 RA Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;
 RT "An overexpressed gene transcript in senescent and quiescent human
 RT fibroblasts encoding a novel protein in the epidermal growth factor-
 RT like repeat family stimulates DNA synthesis.";
 RL Mol. Cell. Biol. 15:120-128(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97001163; PubMed=8812496;
 RA Ikegawa S., Toda T., Okui K., Nakamura Y.;
 RT "Structure and chromosomal assignment of the human S1-5 gene (FBNL)
 RT that is highly homologous to fibrillin.";
 RL Genomics 35:590-592(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20068041; PubMed=10601734;
 RA Giltay R., Timpl R., Kostka G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
 RL Matrix Biol. 18:469-480(1999).
 RN [4]
 RP VARIANT DHRD/MLVT TRP-345, AND VARIANT PHE-220.
 RX MEDLINE=99295941; PubMed=10369267;
 RA Stone E.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,
 RA Vandenburgh K., Cousin P., Nishimura D., Swiderski R.E., Silvestri G.,
 RA Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,
 RA Schorderet D.F.;
 RT "A single EFEMP1 mutation associated with both malattia Leventinese
 RT and Doyme honeycomb retinal dystrophy.";

```

RL  Nat. Genet. 22:199-202(1999).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Comment=Experimental confirmation may be lacking for some
CC      isoforms;
CC      Name=1;
CC      IsoId=Q12805-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q12805-2; Sequence=VSP_001392;
CC      Name=3;
CC      IsoId=Q12805-3; Sequence=VSP_001393;
CC      Name=4;
CC      IsoId=Q12805-4; Sequence=VSP_001394;
CC  -!- DISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB RETINAL
CC      DYSTROPHY (DHRD) ALSO KNOWN AS MALATTIA LEVENTINESE (MLVT' OR ML),
CC      AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY YELLOW-WHITE
CC      DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
CC      PIGMENT EPITHELIUM.
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 6 EGF-like domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U03877; AAA65590.1; -.
DR  HSSP; P35555; 1EMN.
DR  Genew; HGNC:3218; EFEMP1.
DR  MIM; 601548; -.
DR  MIM; 126600; -.
DR  GO; GO:0005578; C:extracellular matrix; TAS.
DR  GO; GO:0007601; P:vision; TAS.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF00008; EGF; 3.
DR  SMART; SM00179; EGF_CA; 4.
DR  PROSITE; PS00010; ASX_HYDROXYL; 4.
DR  PROSITE; PS00022; EGF_1; FALSE_NEG.
DR  PROSITE; PS01186; EGF_2; 4.
DR  PROSITE; PS01187; EGF_CA; 6.
KW  Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal;
KW  Disease mutation; Polymorphism; Alternative splicing.
FT  SIGNAL          1      17      POTENTIAL.
FT  CHAIN           18     493      EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT                                     MATRIX PROTEIN 1.
FT  DOMAIN          26     71      EGF-LIKE 1, DIVERGENT.
FT  DOMAIN          173    213      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          214    253      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          254    293      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          294    333      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          334    378      EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

```

FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	184	199	BY SIMILARITY.
FT	DISULFID	201	212	BY SIMILARITY.
FT	DISULFID	218	228	BY SIMILARITY.
FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1	8	Missing (in isoform 2).
FT				/FTid=VSP_001392.
FT	VARSPLIC	58	58	Missing (in isoform 3).
FT				/FTid=VSP_001393.
FT	VARSPLIC	106	106	Missing (in isoform 4).
FT				/FTid=VSP_001394.
FT	VARIANT	220	220	I -> F.
FT				/FTid=VAR_009512.
FT	VARIANT	345	345	R -> W (IN MVLT).
FT				/FTid=VAR_009513.
SQ	SEQUENCE	493 AA;	54640 MW;	128CA5ED140DF414 CRC64;

Query Match 43.5%; Score 1101; DB 1; Length 493;
 Best Local Similarity 42.0%; Pred. No. 1.6e-74;
 Matches 208; Conservative 69; Mismatches 162; Indels 56; Gaps 8;

Qy	6	RILTVTILALCLPSGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCV	60
		: : : : : : : : : : : : : : :	
Db	3	KALFLTMLTLALVKSQDTEETITYTQCTDGYEWDVPVRQQCKDIDECDIVPDACKGGMKCV	62
Qy	61	NQNGGYLCIPRTNPVY---RGPYSNPY-----STPYSGPYPAA-----	95
		: : : : : : : : : : :	
Db	63	NHYGGYLCPLKTAQIIVNNEQPQETQPAEGTSGATTGVVAASSMATSGVLPGGGFVASA	122
Qy	96	-----APPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATD	134
		: : : : : : : : : : :	
Db	123	AAVAGPEMQTGRNNFVIRRNPAQPRIQCAAGYEQSEHNVCQDIDECTAG	180
Qy	135	SHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCN	193
		: : : : : : : : : : : : : :	
Db	181	THNCRADQVCINLRGSFACQCPGQYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCS	240
Qy	194	PGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF	253
		: : : : : : : : : : : :	
Db	241	PGFQLAANNYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDIDECRT	300
Qy	254	SEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFK	313
		: : : : : : : : : : : : :	
Db	301	SSYLCQYQCVNEPGKFSCMCPQGYQVV-RSRTCQDINECETTNE-CREDEMWNHYHGGR	358
Qy	314	CIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTR	373

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      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db    359 CYPRNPCQDPYILTPENRCVCPVSNAMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTI 418
Qy    374 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRG 433
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db    419 YANTINTFRIKSGNENGEFYLRQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRT 478
Qy    434 SSVIRLRIYVSQYPF 448
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db    479 SSVLRLTIIVGPF SF 493

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RESULT 9

FBL2_MOUSE

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ID    FBL2_MOUSE      STANDARD;          PRT;  1221 AA.
AC    P37889; Q9WUI2;
DT    01-OCT-1994 (Rel. 30, Created)
DT    01-OCT-1994 (Rel. 30, Last sequence update)
DT    15-SEP-2003 (Rel. 42, Last annotation update)
DE    Fibulin-2 precursor.
GN    FBLN2.
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC    TISSUE=Fibroblast;
RX    MEDLINE=94064787; PubMed=8245130;
RA    Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT    "Structure and expression of fibulin-2, a novel extracellular matrix
RT    protein with multiple EGF-like repeats and consensus motifs for
RT    calcium binding.";
RL    J. Cell Biol. 123:1269-1277(1993).
RN    [2]
RP    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX    MEDLINE=99337686; PubMed=10406956;
RA    Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT    "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT    characterization.";
RL    Eur. J. Biochem. 263:471-477(1999).
RN    [3]
RP    DEVELOPMENTAL STAGE.
RX    PubMed=8850569;
RA    Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT    "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT    developing mouse embryo.";
RL    Dev. Dyn. 205:348-364(1996).
RN    [4]
RP    BINDING TO LAMA2.
RX    PubMed=10022829;
RA    Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT    "Binding of the G domains of laminin alpha1 and alpha2 chains and
RT    perlecan to heparin, sulfatides, alpha-dystroglycan and several
RT    extracellular matrix proteins.";
RL    EMBO J. 18:863-870(1999).
RN    [5]

```

RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX PubMed=11737251;
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
 CC CALCIUM DEPENDENT.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P37889-1; Sequence=Displayed;
 CC Name=2; Synonyms=EGF3-less;
 CC IsoId=P37889-2; Sequence=VSP_001391;
 CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
 CC connective tissues.
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
 CC family contributes to the formation of molecularly distinct
 CC extracellular matrices already during early developmental stages
 CC of a large number of tissues.
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 11 EGF-like domains.
 CC -----
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 CC -----
 DR EMBL; X75285; CAA53040.1; -.
 DR EMBL; AF135253; AAD34456.1; -.
 DR EMBL; AF135239; AAD34456.1; JOINED.
 DR EMBL; AF135240; AAD34456.1; JOINED.
 DR EMBL; AF135241; AAD34456.1; JOINED.
 DR EMBL; AF135242; AAD34456.1; JOINED.
 DR EMBL; AF135243; AAD34456.1; JOINED.
 DR EMBL; AF135244; AAD34456.1; JOINED.
 DR EMBL; AF135245; AAD34456.1; JOINED.
 DR EMBL; AF135246; AAD34456.1; JOINED.
 DR EMBL; AF135247; AAD34456.1; JOINED.
 DR EMBL; AF135248; AAD34456.1; JOINED.
 DR EMBL; AF135249; AAD34456.1; JOINED.
 DR EMBL; AF135250; AAD34456.1; JOINED.
 DR EMBL; AF135251; AAD34456.1; JOINED.
 DR EMBL; AF135252; AAD34456.1; JOINED.
 DR PIR; A49457; A49457.
 DR HSSP; P00736; 1APQ.
 DR MGD; MGI:95488; Fbln2.
 DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF_CA; 10.
 KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 KW Calcium-binding; Alternative splicing; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 27 1221 FIBULIN-2.
 FT DOMAIN 27 434 N.
 FT DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).
 FT DOMAIN 177 434 SUBDOMAIN NB (CYS-FREE).
 FT DOMAIN 435 477 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 478 510 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 511 543 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 594 635 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 669 708 EGF-LIKE 2.
 FT DOMAIN 709 755 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 756 800 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 801 846 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 847 894 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 895 937 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 938 979 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 980 1018 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1019 1061 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1062 1106 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1111 1221 DOMAIN III.
 FT SITE 421 423 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 435 462 BY SIMILARITY.
 FT DISULFID 436 469 BY SIMILARITY.
 FT DISULFID 449 470 BY SIMILARITY.
 FT DISULFID 479 508 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT DISULFID 511 535 BY SIMILARITY.
 FT DISULFID 512 542 BY SIMILARITY.
 FT DISULFID 525 543 BY SIMILARITY.
 FT DISULFID 598 610 BY SIMILARITY.
 FT DISULFID 606 619 BY SIMILARITY.
 FT DISULFID 621 634 BY SIMILARITY.
 FT DISULFID 673 683 BY SIMILARITY.
 FT DISULFID 679 692 BY SIMILARITY.
 FT DISULFID 694 707 BY SIMILARITY.
 FT DISULFID 713 726 BY SIMILARITY.
 FT DISULFID 720 735 BY SIMILARITY.
 FT DISULFID 742 754 BY SIMILARITY.
 FT DISULFID 805 818 BY SIMILARITY.
 FT DISULFID 812 827 BY SIMILARITY.
 FT DISULFID 833 845 BY SIMILARITY.
 FT DISULFID 899 912 BY SIMILARITY.

FT	DISULFID	906	921	BY SIMILARITY.
FT	DISULFID	923	936	BY SIMILARITY.
FT	DISULFID	942	954	BY SIMILARITY.
FT	DISULFID	950	963	BY SIMILARITY.
FT	DISULFID	965	978	BY SIMILARITY.
FT	DISULFID	984	993	BY SIMILARITY.
FT	DISULFID	989	1002	BY SIMILARITY.
FT	DISULFID	1004	1017	BY SIMILARITY.
FT	DISULFID	1023	1035	BY SIMILARITY.
FT	DISULFID	1031	1044	BY SIMILARITY.
FT	DISULFID	1046	1060	BY SIMILARITY.
FT	DISULFID	1066	1079	BY SIMILARITY.
FT	DISULFID	1073	1088	BY SIMILARITY.
FT	DISULFID	1093	1105	BY SIMILARITY.
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	497	497	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	737	737	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1072	1072	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	709	755	Missing (in isoform 2).
FT				/FTId=VSP_001391.
FT	CONFLICT	140	159	HSGRKYAAGHTVHLSSCRAC -> TVAVSICWPYRPPLILP
FT				GF (IN REF. 2).
FT	CONFLICT	348	348	S -> L (IN REF. 2).
FT	CONFLICT	507	507	Q -> QQ (IN REF. 2).
FT	CONFLICT	1102	1102	Q -> E (IN REF. 2).
SQ	SEQUENCE	1221	AA; 131818	MW; 87DB2A10A8FDC45F CRC64;

Qy	23	AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSN	82
Db	829	ARQRCMDGF-LQDPEGNCVDINECTSLLEPCRSRGFSCINTVGSYTC-----	873
Qy	83	PYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPT	141
Db	874	-----QRNPLVCGRGYHANEEGSECDVNECETGVHRCGEG	909
Qy	142	QICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGF	196
Db	910	QLCYNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSAAGF	969
Qy	197	TLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSE	255
Db	970	LLAADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAG	1028
Qy	256	FLCQHECVNQPGTYFCSCP-PGYIILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKC	314
Db	1029	ILCTFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEABTCHNIQGSFRC	1088
Qy	315	IDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQM	368
Db	1089	L-RFDCPPNYVRVSQTKC---ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRI	1143
Qy	369	QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM	422

RESULT 10

FBL1_CERAE

ID FBL1_CERAE STANDARD; PRT; 598 AA.
AC Q8MJJ9;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1C (Fragment).
GN FBLN1.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A., AND INTERACTION WITH DTR.
RX PubMed=11846885;
RA Brooke J.S., Cha J.-H., Eidels L.;
RT "Latent transforming growth factor beta-binding protein-3 and
RT fibulin-1C interact with the extracellular domain of the
RT heparin-binding EGF-like growth factor precursor.";
RL BMC Cell Biol. 3:2-2(2002).
CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC May play a role in cell adhesion and migration along protein
CC fibers within the extracellular matrix (ECM). Could be important
CC for certain developmental processes and contribute to the
CC supramolecular organization of ECM architecture, in particular to
CC those of basement membranes. May serve to anchor the
CC mature/soluble form of DTR to its fibers as it migrates through
CC the extracellular matrix. The direct physical association with DTR
CC may be useful in such tissue developmental processes as wound
CC healing.
CC -!- SUBUNIT: Interacts with itself and with various extracellular
CC matrix components (By similarity). Interacts with the
CC mature/soluble form of DTR.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains at least 2 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 9 EGF-like domains.
CC -----
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CC -----
DR EMBL; AF395659; AAM90567.1; -.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.

DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 5.
 DR SMART; SM00104; ANATO; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 7.
 KW Glycoprotein; Extracellular matrix; Repeat; EGF-like domain;
 KW Calcium-binding.
 FT NON_TER 1 1
 FT CHAIN <1 598 FIBULIN-1C.
 FT DOMAIN <1 27 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 28 60 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 92 131 EGF-LIKE 1.
 FT DOMAIN 132 177 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 178 223 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 224 270 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 271 313 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 314 355 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 356 395 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 396 439 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 440 484 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 271 355 SELF-ASSOCIATION AND FN1-BINDING (BY
 FT SIMILARITY).
 FT DISULFID <1 25 BY SIMILARITY.
 FT DISULFID 7 26 BY SIMILARITY.
 FT DISULFID 28 52 BY SIMILARITY.
 FT DISULFID 29 59 BY SIMILARITY.
 FT DISULFID 42 60 BY SIMILARITY.
 FT DISULFID 96 106 BY SIMILARITY.
 FT DISULFID 102 115 BY SIMILARITY.
 FT DISULFID 117 130 BY SIMILARITY.
 FT DISULFID 136 149 BY SIMILARITY.
 FT DISULFID 143 158 BY SIMILARITY.
 FT DISULFID 164 176 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 189 204 BY SIMILARITY.
 FT DISULFID 210 222 BY SIMILARITY.
 FT DISULFID 228 242 BY SIMILARITY.
 FT DISULFID 257 270 BY SIMILARITY.
 FT DISULFID 275 288 BY SIMILARITY.
 FT DISULFID 282 297 BY SIMILARITY.
 FT DISULFID 299 312 BY SIMILARITY.
 FT DISULFID 318 330 BY SIMILARITY.
 FT DISULFID 326 339 BY SIMILARITY.
 FT DISULFID 341 354 BY SIMILARITY.
 FT DISULFID 360 369 BY SIMILARITY.
 FT DISULFID 365 378 BY SIMILARITY.
 FT DISULFID 380 394 BY SIMILARITY.
 FT DISULFID 400 413 BY SIMILARITY.
 FT DISULFID 409 422 BY SIMILARITY.
 FT DISULFID 424 438 BY SIMILARITY.
 FT DISULFID 444 457 BY SIMILARITY.
 FT DISULFID 451 466 BY SIMILARITY.

FT DISULFID 471 483 BY SIMILARITY.
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 598 AA; 65516 MW; 849BF018DF452B02 CRC64;

Query Match 28.7%; Score 728; DB 1; Length 598;
 Best Local Similarity 34.8%; Pred. No. 8e-47;
 Matches 158; Conservative 76; Mismatches 188; Indels 32; Gaps 16;

Qy 16 CLPSPGNAQAQ----CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR 71
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 149 CINTVGSFRCQRDSSCGTGYEL-TEDNSCKDIDQCESGIHNCLPDFICQNTLGSFRCRKP 207

Qy 72 ---TNPVYRGYPYNSPYS-----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDEN 123
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 208 LQCKNGFIQDALANCIDINECLSVSAPCPTGHTCINTEGSYQKNVPNCGRGYHLNEEG 267

Qy 124 QCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQ 178
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 268 TRCDVNECAPPAEPCGKGHRCVNSPGSFRCECKTGYFDGISRMCVDVNECQRYPGRLCG 327

Qy 179 QLCANVPGSYSCTCNPGFTLNEEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYEL 238
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 328 HKCENTLGSYVCSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQL 386

Qy 239 EE-DGVHCSMDDECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEH 294
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 387 SDVDGVTCEDIDECALPTGGHICSYRCINIPGSFQCSCPASGYRLAPNGRNCQDIDECVT 446

Qy 295 RNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRD 352
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 447 GIHNCSINETCFNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKLPRLITYYH 505

Qy 353 MDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKG 412
 : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 506 LSFPTNIQAPAVVFRMGPSAVPGDSMQLAITGNEEGFFTRKVSPhSGVVALTKPVPE 565

Qy 413 PREIQLDLEM--ITVNTVINFRGSSVIRLRIYVS 444
 | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
 Db 566 PRDLLLTVKMDLYRHGTVSSF----VAKLFIFVS 595

RESULT 11

FBL1_CHICK

ID FBL1_CHICK STANDARD; PRT; 704 AA.
 AC 073775; 073774;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1 precursor.
 GN FBLN1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

```

RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS C AND D).
RC      TISSUE=Embryo;
RX      MEDLINE=99120531; PubMed=9923656;
RA      Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT      "Identification of chicken and C. elegans fibulin-1 homologs and
RT      characterization of the C. elegans fibulin-1 gene.";
RL      Matrix Biol. 17:635-646(1998).
CC      -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC      May play a role in cell adhesion and migration along protein
CC      fibers within the extracellular matrix (ECM). Could be important
CC      for certain developmental processes and contribute to the
CC      supramolecular organization of ECM architecture, in particular to
CC      those of basement membranes.
CC      -!- SUBUNIT: Interacts with itself and with various extracellular
CC      matrix components (By similarity).
CC      -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=D;
CC      IsoId=O73775-2; Sequence=Displayed;
CC      Name=C;
CC      IsoId=O73775-1; Sequence=VSP_007378;
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC      -!- SIMILARITY: Contains 9 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF051399; AAC05387.1; -.
DR      EMBL; AF051400; AAC05388.1; -.
DR      HSSP; P00742; 1HCG.
DR      InterPro; IPR000020; Anaphylatoxin.
DR      InterPro; IPR000152; Asx_hydroxyl.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      Pfam; PF01821; ANATO; 2.
DR      Pfam; PF00008; EGF; 6.
DR      SMART; SM00104; ANATO; 3.
DR      SMART; SM00181; EGF; 9.
DR      SMART; SM00179; EGF_CA; 8.
DR      PROSITE; PS00010; ASX_HYDROXYL; 5.
DR      PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR      PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR      PROSITE; PS00022; EGF_1; FALSE_NEG.
DR      PROSITE; PS01186; EGF_2; 3.
DR      PROSITE; PS01187; EGF_CA; 8.
KW      Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW      Repeat; EGF-like domain; Calcium-binding.
FT      SIGNAL          1      25      POTENTIAL.
FT      CHAIN           26     704      FIBULIN-1.

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FT	DOMAIN	33	74	ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	75	109	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	110	142	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	177	216	EGF-LIKE 1.
FT	DOMAIN	217	262	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	263	308	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	309	356	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	357	399	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	400	441	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	442	481	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	482	525	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	526	579	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	357	441	SELF-ASSOCIATION AND FN1-BINDING (BY
FT				SIMILARITY).
FT	DISULFID	33	59	BY SIMILARITY.
FT	DISULFID	34	66	BY SIMILARITY.
FT	DISULFID	47	67	BY SIMILARITY.
FT	DISULFID	76	107	BY SIMILARITY.
FT	DISULFID	89	108	BY SIMILARITY.
FT	DISULFID	110	134	BY SIMILARITY.
FT	DISULFID	111	141	BY SIMILARITY.
FT	DISULFID	124	142	BY SIMILARITY.
FT	DISULFID	181	191	BY SIMILARITY.
FT	DISULFID	187	200	BY SIMILARITY.
FT	DISULFID	202	215	BY SIMILARITY.
FT	DISULFID	221	234	BY SIMILARITY.
FT	DISULFID	228	243	BY SIMILARITY.
FT	DISULFID	249	261	BY SIMILARITY.
FT	DISULFID	267	280	BY SIMILARITY.
FT	DISULFID	274	289	BY SIMILARITY.
FT	DISULFID	295	307	BY SIMILARITY.
FT	DISULFID	313	326	BY SIMILARITY.
FT	DISULFID	320	335	BY SIMILARITY.
FT	DISULFID	342	355	BY SIMILARITY.
FT	DISULFID	361	374	BY SIMILARITY.
FT	DISULFID	368	383	BY SIMILARITY.
FT	DISULFID	385	398	BY SIMILARITY.
FT	DISULFID	404	416	BY SIMILARITY.
FT	DISULFID	412	425	BY SIMILARITY.
FT	DISULFID	427	440	BY SIMILARITY.
FT	DISULFID	446	455	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	DISULFID	466	480	BY SIMILARITY.
FT	DISULFID	486	499	BY SIMILARITY.
FT	DISULFID	495	508	BY SIMILARITY.
FT	DISULFID	510	524	BY SIMILARITY.
FT	DISULFID	530	543	BY SIMILARITY.
FT	DISULFID	537	552	BY SIMILARITY.
FT	DISULFID	557	578	BY SIMILARITY.
FT	CARBOHYD	96	96	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	536	536	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	540	540	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	568	704	VRLEKTDITRICKSCRPNVDVNCVLDPVHTISHTVISLPTFR
FT				EFTRPEEIIFLRAITPTYPANQADIIIDITEGNLRESFDII
FT				KRYMDGMTVGVRQVRPIVGPFHAILKLEMNYVMGGVVSHR
FT				NI NVHIFVSEYWF -> RCERLPCNENKECQSLPLRITYY
FT				HLSFPTNIQVPTDIFRMGPSNAVPGDKILLSIISGNQEGFF

FT TTKKVNNHSGIVVMQRQITEPRDLLLTIQMLTRHGTVNTF
 FT IAKLFVVFVSAQL (in isoform C).
 FT /FTid=VSP_007378.
 SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;

Query Match 28.5%; Score 722; DB 1; Length 704;
 Best Local Similarity 34.6%; Pred. No. 2.6e-46;
 Matches 163; Conservative 68; Mismatches 158; Indels 82; Gaps 22;

Qy 15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP 70
 :| :||: : || || | | :||:| : | :|| :| |
 Db 279 ICQNTPGSFRCRPKLQCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-Q 336
 Qy 71 RTNPVYRGYPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD-SNQCVDVD 129
 | :| | || :| :|||
 Db 337 RISP-----SCGRGYHLNEDGTRCVDVD 359
 Qy 130 ECATDSHQCNPTQICINTEGGYTCSTDGYW--LLEGQCLDIDECRY---GYCQQLCANV 184
 ||:| :||| | | | || :| :||:| | | |
 Db 360 ECSSSDQPCGEGHVCEINGPGNYRCECKSGYSFQVSRCTCIDINECRYPGRCAHKCENT 419
 Qy 185 PGYSYCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGV 243
 |||| || | : ||||:| : || | | ||| : | :|| : ||:
 Db 420 PGYYCTCTMGFKLSSDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDGI 478
 Qy 244 HCSDMDECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCN 300
 | :|||: :| :| ||:| :|| || | :| :|||:| | | :
 Db 479 SCEDIDECALPTGGHICSFRCINIPGSFQCTCPSTGYRLAPNARNQCQDIDECVAETHNCS 538
 Qy 301 LQOTCYNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFIT 348
 :||:|:| |||:| : | | : | ||: | : | | ||
 Db 539 FNETCFNIQGGFRCLS-LECPENYRKSGDTRVLEKTDTRICIKSCRPNVNCVLDPVHTI 597
 Qy 349 LYRDMDVVSGRSV--PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTG 398
 : : : | :| :| | || | || | || | || |
 Db 598 SHTVISLPTFREFTRPEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DG 655
 Qy 399 PISATLVMTRPIKGPRIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
 : ||| || | ||| : ||:| :||:| |
 Db 656 MTVGVVVRQVRPIVGPFHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF 704

RESULT 12

FBL2_HUMAN

ID FBL2_HUMAN STANDARD; PRT; 1184 AA.

AC P98095;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Fibulin-2 precursor.

GN FBLN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fibroblast;
 RX MEDLINE=95104855; PubMed=7806230;
 RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,
 RA Chu M.-L.;
 RT "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
 RT of the gene on human and mouse chromosomes.";
 RL Genomics 22:425-430(1994).
 RN [2]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8737292;
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
 RT early human embryo.";
 RL Histochem. J. 28:109-116(1996).
 CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
 CC CALCIUM DEPENDENT.
 CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
 CC connective tissues. Expressed in heart, placenta and ovary.
 CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
 CC development. Primarily detected within the neuropithelium, spinal
 CC ganglia and peripheral nerves.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 11 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC -----
 DR EMBL; X82494; CAA57876.1; -.
 DR PIR; A55184; A55184.
 DR HSSP; P00736; 1APQ.
 DR Genew; HGNC:3601; FBLN2.
 DR MIM; 135821; -.
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005509; F:calcium ion binding activity; TAS.
 DR GO; GO:0005207; F:extracellular matrix glycoprotein; TAS.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF00008; EGF; 7.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 5.

DR	PROSITE; PS01187; EGF_CA; 9.			
KW	Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;			
KW	Calcium-binding; Repeat.			
FT	SIGNAL	1	27	POTENTIAL.
FT	CHAIN	28	1184	FIBULIN-2.
FT	DOMAIN	28	444	N.
FT	DOMAIN	28	177	SUBDOMAIN NA (CYS-RICH).
FT	DOMAIN	178	444	SUBDOMAIN NB (CYS-FREE).
FT	DOMAIN	445	480	ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	488	519	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	521	553	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	604	645	EGF-LIKE 1, CALCIUM-BINDING.
FT	DOMAIN	679	718	EGF-LIKE 2.
FT	DOMAIN	719	763	EGF-LIKE 3, CALCIUM-BINDING.
FT	DOMAIN	764	809	EGF-LIKE 4, CALCIUM-BINDING.
FT	DOMAIN	810	857	EGF-LIKE 5, CALCIUM-BINDING.
FT	DOMAIN	858	900	EGF-LIKE 6, CALCIUM-BINDING.
FT	DOMAIN	901	942	EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	943	981	EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	982	1024	EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	1025	1069	EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	1070	1184	DOMAIN III.
FT	DISULFID	445	472	BY SIMILARITY.
FT	DISULFID	446	479	BY SIMILARITY.
FT	DISULFID	459	480	BY SIMILARITY.
FT	DISULFID	489	518	BY SIMILARITY.
FT	DISULFID	502	519	BY SIMILARITY.
FT	DISULFID	521	545	BY SIMILARITY.
FT	DISULFID	522	552	BY SIMILARITY.
FT	DISULFID	535	553	BY SIMILARITY.
FT	DISULFID	608	620	BY SIMILARITY.
FT	DISULFID	616	629	BY SIMILARITY.
FT	DISULFID	631	644	BY SIMILARITY.
FT	DISULFID	683	693	BY SIMILARITY.
FT	DISULFID	689	702	BY SIMILARITY.
FT	DISULFID	704	717	BY SIMILARITY.
FT	DISULFID	723	736	BY SIMILARITY.
FT	DISULFID	730	745	BY SIMILARITY.
FT	DISULFID	751	762	BY SIMILARITY.
FT	DISULFID	768	781	BY SIMILARITY.
FT	DISULFID	775	790	BY SIMILARITY.
FT	DISULFID	796	808	BY SIMILARITY.
FT	DISULFID	814	827	BY SIMILARITY.
FT	DISULFID	821	836	BY SIMILARITY.
FT	DISULFID	843	856	BY SIMILARITY.
FT	DISULFID	862	875	BY SIMILARITY.
FT	DISULFID	869	884	BY SIMILARITY.
FT	DISULFID	886	899	BY SIMILARITY.
FT	DISULFID	905	917	BY SIMILARITY.
FT	DISULFID	913	926	BY SIMILARITY.
FT	DISULFID	928	941	BY SIMILARITY.
FT	DISULFID	947	956	BY SIMILARITY.
FT	DISULFID	952	965	BY SIMILARITY.
FT	DISULFID	967	980	BY SIMILARITY.
FT	DISULFID	986	998	BY SIMILARITY.
FT	DISULFID	994	1007	BY SIMILARITY.
FT	DISULFID	1009	1023	BY SIMILARITY.

FT	DISULFID	1029	1042	BY SIMILARITY.
FT	DISULFID	1036	1051	BY SIMILARITY.
FT	DISULFID	1056	1068	BY SIMILARITY.
FT	CARBOHYD	180	180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	507	507	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1035	1035	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1184 AA;	126543 MW;	CA48490A55F9EC5D CRC64;

Qy	15	LCLPLSPGN---AAQACQTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP	70
Db	780	LCQNTKGSFYCQARQRCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC--	836
Qy	71	RTNPVYRGPPYSNPYSTPYSGPYAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD	129
Db	837	-----QRNPLICARGYHASDDGAKCVDVN	860
Qy	130	ECATDSHQCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANV	184
Db	861	ECETGVHRCGEGQVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENT	920
Qy	185	PGSYSCTCNPGFITLNEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH	244
Db	921	LGSYRCSACASGFLLAADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT	979
Qy	245	CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ	302
Db	980	CTDIDECAQGAGILCTFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEA	1039
Qy	303	QTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV	356
Db	1040	ETCHNIQGSFRCL-RFECPPNYVQVSKTKC----ERTTCHDFLECQNSPARITHYQLNFO	1094
Qy	357	SGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI	416
Db	1095	TGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLQRAVLEPRDF	1154
Qy	417	QLDLEM	422
Db	1155	ALDVEM	1160

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX MEDLINE=91100426; PubMed=2269669;
 RA Argraves W.S., Tran H., Burgess W.H., Dickerson K.;
 RT "Fibulin is an extracellular matrix and plasma glycoprotein with
 RT repeated domain structure.";
 RL J. Cell Biol. 111:3155-3164(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM D), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH FN1 AND FGB.
 RX PubMed=9106159;
 RA Tran H., Mattei M., Godyna S., Argraves W.S.;
 RT "Human fibulin-1D: molecular cloning, expression and similarity with
 RT S1-5 protein, a new member of the fibulin gene family.";
 RL Matrix Biol. 15:479-493(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM D).
 RX MEDLINE=99253993; PubMed=10318851;
 RA Krichevsky A.M., Metzger E., Rosen H.;
 RT "Translational control of specific genes during differentiation of
 RT HL-60 cells.";
 RL J. Biol. Chem. 274:14295-14305(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human cDNA clones with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlffing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Spl and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [8]
 RP SEQUENCE OF 30-44.
 RX MEDLINE=89354537; PubMed=2527614;
 RA Argraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;
 RT "Fibulin, a novel protein that interacts with the fibronectin
 RT receptor beta subunit cytoplasmic domain.";

RL Cell 58:623-629(1989).
 RN [9]
 RP SELF-ASSOCIATION AND INTERACTION WITH FN1.
 RX PubMed=1400330;
 RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
 RA Argraves W.S.;
 RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
 RT region of fibronectin.";
 RL J. Biol. Chem. 267:20120-20125(1992).
 RN [10]
 RP POSSIBLE FUNCTION.
 RX PubMed=7534784;
 RA Roark E.F., Keene D.R., Haudenschild C.C., Godyna S., Little C.D.,
 RA Argraves W.S.;
 RT "The association of human fibulin-1 with elastic fibers: an
 RT immunohistological, ultrastructural, and RNA study.";
 RL J. Histochem. Cytochem. 43:401-411(1995).
 RN [11]
 RP INTERACTION WITH FGB.
 RX PubMed=7642629;
 RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
 RA Argraves W.S.;
 RT "The interaction of fibulin-1 with fibrinogen. A potential role in
 RT hemostasis and thrombosis.";
 RL J. Biol. Chem. 270:19458-19464(1995).
 RN [12]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8737292;
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
 RT early human embryo.";
 RL Histochem. J. 28:109-116(1996).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=96133928; PubMed=8552629;
 RA Clinton G.M., Rougeot C., Derancourt J., Roger P., Defrenne A.,
 RA Godyna S., Argraves W.S., Rochefort H.;
 RT "Estrogens increase the expression of fibulin-1, an extracellular
 RT matrix protein secreted by human ovarian cancer cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:316-320(1996).
 RN [14]
 RP CALCIUM, SELF-ASSOCIATION, AND FN1-BINDING SITES.
 RX PubMed=9278415;
 RA Tran H., VanDusen W.J., Argraves W.S.;
 RT "The self-association and fibronectin-binding sites of fibulin-1 map
 RT to calcium-binding epidermal growth factor-like domains.";
 RL J. Biol. Chem. 272:22600-22606(1997).
 RN [15]
 RP ROLE IN TUMOR FORMATION AND INVASION.
 RX PubMed=9393974;
 RA Qing J., Maher V.M., Tran H., Argraves W.S., Dunstan R.W.,
 RA McCormick J.J.;
 RT "Suppression of anchorage-independent growth and matrigel invasion and
 RT delayed tumor formation by elevated expression of fibulin-1D in human
 RT fibrosarcoma-derived cell lines.";
 RL Oncogene 15:2159-2168(1997).
 RN [16]

RESULT 14

FBL1_MOUSE

ID FBL1_MOUSE STANDARD; PRT; 705 AA.
AC Q08879; Q08878; Q8C3B1; Q91ZC9; Q922K8;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor (Basement-membrane protein 90) (BM-90).
GN FBLN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS C AND D), AND LIGANDS INTERACTION.
RX MEDLINE=93358897; PubMed=8354280;
RA Pan T.-C., Kluge M., Zhang R.Z., Mayer U., Timpl R., Chu M.-L.;
RT "Sequence of extracellular mouse protein BM-90/fibulin and its
calcium-dependent binding to other basement-membrane ligands.";
RL Eur. J. Biochem. 215:733-740(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC STRAIN=C57BL/6J; TISSUE=Head, and Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM C).
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [5]
 RP CHARACTERIZATION OF NID AFFINITY.
 RX PubMed=7844816;
 RA Sasaki T., Kostka G., Goehring W., Wiedemann H., Mann K., Chu M.-L.,
 RA Timpl R.;
 RT "Structural characterization of two variants of fibulin-1 that differ
 RT in nidogen affinity.";
 RL J. Mol. Biol. 245:241-250(1995).
 RN [6]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8850569;
 RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
 RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
 RT developing mouse embryo.";
 RL Dev. Dyn. 205:348-364(1996).
 RN [7]
 RP NID-BINDING SITE.
 RC STRAIN=129/Sv;
 RX PubMed=9299350;
 RA Adam S., Goehring W., Wiedemann H., Chu M.-L., Timpl R., Kostka G.;
 RT "Binding of fibulin-1 to nidogen depends on its C-terminal globular
 RT domain and a specific array of calcium-binding epidermal growth
 RT factor-like (EG) modules.";
 RL J. Mol. Biol. 272:226-236(1997).
 RN [8]
 RP BINDING TO LAMA2.
 RX PubMed=10022829;
 RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
 RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
 RT perlecan to heparin, sulfatides, alpha-dystroglycan and several

RT extracellular matrix proteins.";
 RL EMBO J. 18:863-870(1999).
 RN [9]
 RP INTERACTION WITH AGC1 AND CSPG2.
 RX PubMed=10400671;
 RA Aspberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 RT versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 RN [10]
 RP INTERACTION WITH NID.
 RX PubMed=11589703;
 RA Ries A., Goehring W., Fox J.W., Timpl R., Sasaki T.;
 RT "Recombinant domains of mouse nidogen-1 and their binding to basement
 RT membrane proteins and monoclonal antibodies.";
 RL Eur. J. Biochem. 268:5119-5128(2001).
 RN [11]
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX PubMed=11737251;
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 RN [12]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX PubMed=11238726;
 RA Ohsawa I., Takamura C., Kohsaka S.;
 RT "Fibulin-1 binds the amino-terminal head of beta-amyloid precursor
 RT protein and modulates its physiological function.";
 RL J. Neurochem. 76:1411-1420(2001).
 RN [13]
 RP INTERACTION WITH E6, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
 RX PubMed=12200142;
 RA Du M., Fan X., Hong E., Chen J.J.;
 RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
 RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
 RN [14]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=11836357;
 RA Debeer P., Schoenmakers E.F.P.M., Twal W.O., Argraves W.S.,
 RA De Smet L., Fryns J.-P., Van De Ven W.J.M.;
 RT "The fibulin-1 gene (FBLN1) is disrupted in a t(12;22) associated with
 RT a complex type of synpolydactyly.";
 RL J. Med. Genet. 39:98-104(2002).
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
 CC May play a role in cell adhesion and migration along protein
 CC fibers within the extracellular matrix (ECM). Could be important
 CC for certain developmental processes and contribute to the
 CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components such as FN1, LAMA1, LMA2, NID, AGC1, CSPG2 and
 CC type IV collagen. Interacts also with papillomavirus E6 proteins.
 CC Binding analysis demonstrated for isoform C a 100-fold stronger
 CC binding to the basement membrane protein NID than for isoform D.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:


```

      :|:| | |:|: | | | | :| | | | : | | | | : : :
Db      545 FNIQGSFRCLS-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVI 603

Qy      354 DVVSGRSV--PADIFQMATT-RYPG--AYYIFQIKSGNEGREFYM--RQTGPISATLV 405
      : : | | :| :| | | | | | | | | : : | :
Db      604 SLPTFREFTRP EEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGQVR 663

Qy      406 MTRPIKGPRIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
      ||| | | | | | : | :| : : | :| :| |
Db      664 QVRPIVGPFYAVLKLEMNYVLGGVVSHR--NVVNVHIFVSEYWF 705

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RESULT 15

FBL1_BRARE

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ID      FBL1_BRARE      STANDARD;      PRT;      681 AA.
AC      O42182; O42183;
DT      15-SEP-2003 (Rel. 42, Created)
DT      15-SEP-2003 (Rel. 42, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibulin-1 precursor.
GN      FBLN1.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS C AND D).
RA      Zhang H.-Y., Lardelli M., Ekblom P.;
RT      "Sequence of zebrafish fibulin-1 and its expression in developing
RT      heart and other embryonic organs.";
RL      Dev. Genes Evol. 207:340-351(1997).
CC      -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC      May play a role in cell adhesion and migration along protein
CC      fibers within the extracellular matrix (ECM). Could be important
CC      for certain developmental processes and contribute to the
CC      supramolecular organization of ECM architecture, in particular to
CC      those of basement membranes.
CC      -!- SUBUNIT: Interacts with itself and with various extracellular
CC      matrix components such as FN1, LAMA1, NID, AGC1 and CSPG2.
CC      -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=D;
CC      IsoId=O42182-1; Sequence=Displayed;
CC      Name=C;
CC      IsoId=O42182-2; Sequence=VSP_007379;
CC      -!- DEVELOPMENTAL STAGE: Isoform C is detected in the later blastula
CC      period, 4 h after fertilization. Isoform D is not detected at this
CC      stage, it first appears during the gastrula period in 8-h-old
CC      embryos. Expression of both isoforms is then maintained throughout
CC      development. During later developmental stages, prominent
CC      expression is seen in regions where tissue compartments are
CC      continuously moving in relation to each other.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC      -!- SIMILARITY: Contains 9 EGF-like domains.

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CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AF013751; AAB80944.1; -.
DR EMBL; AF013752; AAB80945.1; -.
DR HSSP; P35555; 1EMN.
DR ZFIN; ZDB-GENE-990415-73; fbln1.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001673; S_mold_repeat.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF00008; EGF; 4.
DR SMART; SM00104; ANATO; 2.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 6.
KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW Repeat; EGF-like domain; Calcium-binding.
FT SIGNAL      1      17      POTENTIAL.
FT CHAIN       18     681      FIBULIN-1.
FT DOMAIN      29      63      ANAPHYLATOXIN-LIKE 1.
FT DOMAIN      68     107      ANAPHYLATOXIN-LIKE 2.
FT DOMAIN     108     139      ANAPHYLATOXIN-LIKE 3.
FT DOMAIN     158     192      EGF-LIKE 1.
FT DOMAIN     193     238      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     239     284      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     285     331      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     332     373      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     374     415      EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     416     455      EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     456     499      EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN     500     554      EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DISULFID    29      55      BY SIMILARITY.
FT DISULFID    30      62      BY SIMILARITY.
FT DISULFID    43      63      BY SIMILARITY.
FT DISULFID    72     103      BY SIMILARITY.
FT DISULFID    85     104      BY SIMILARITY.
FT DISULFID   106     125      BY SIMILARITY.
FT DISULFID   107     138      BY SIMILARITY.
FT DISULFID   114     139      BY SIMILARITY.
FT DISULFID   162     171      BY SIMILARITY.
FT DISULFID   167     176      BY SIMILARITY.
FT DISULFID   178     191      BY SIMILARITY.
FT DISULFID   197     210      BY SIMILARITY.
FT DISULFID   204     219      BY SIMILARITY.
FT DISULFID   225     237      BY SIMILARITY.

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FT	DISULFID	243	256	BY SIMILARITY.
FT	DISULFID	250	265	BY SIMILARITY.
FT	DISULFID	271	283	BY SIMILARITY.
FT	DISULFID	289	301	BY SIMILARITY.
FT	DISULFID	317	330	BY SIMILARITY.
FT	DISULFID	336	348	BY SIMILARITY.
FT	DISULFID	343	357	BY SIMILARITY.
FT	DISULFID	359	372	BY SIMILARITY.
FT	DISULFID	378	390	BY SIMILARITY.
FT	DISULFID	386	399	BY SIMILARITY.
FT	DISULFID	401	414	BY SIMILARITY.
FT	DISULFID	420	429	BY SIMILARITY.
FT	DISULFID	440	454	BY SIMILARITY.
FT	DISULFID	460	473	BY SIMILARITY.
FT	DISULFID	469	482	BY SIMILARITY.
FT	DISULFID	484	498	BY SIMILARITY.
FT	DISULFID	504	517	BY SIMILARITY.
FT	DISULFID	511	526	BY SIMILARITY.
FT	DISULFID	531	553	BY SIMILARITY.
FT	CARBOHYD	173	173	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	542	681	RPRVDRADIIRCVKSCQHNDISCVLNPILSHSHTAISLPTF
FT				REFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSF
FT				DIIRLDHGMIVGVVKQVRPLVGPVRTVLKLANNYVTNGV
FT				SHRNIINVRIYVSEFWF -> RCERLSCNESNECMAFTRRI
FT				TTYQLTFPAKIPVPTDLFRMGPSNTALGDDIEVAIVDGNRD
FT				GFFAAKRLDHGGVLVLQKPIAWPQDFQIALEMKLKRFGLS
FT				IYLFKIRPVRHARRHQORY (in isoform C).
FT				/FTid=VSP_007379.
SQ	SEQUENCE	681 AA;	74459 MW;	175C966305A46699 CRC64;

Query Match 24.9%; Score 631; DB 1; Length 681;
 Best Local Similarity 32.6%; Pred. No. 1.4e-39;
 Matches 153; Conservative 65; Mismatches 162; Indels 90; Gaps 22;

Qy	16	CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV	75
Db	265	CRP-----RMQCAAGFIQD-ALGSCIDINECVSVTALSRG-QMCFNTVGSFICQRHS---	314
Qy	76	YRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDDVDECATD	134
Db	315	-----VTCGRGYHLNAEGTRCVDIDECAGP	339
Qy	135	SHQCNPTQICINTEGGYTCSDTGYWL--LEGQCLDIDECRYGY---CQQLCANVPGSY	188
Db	340	DNSCD-GHGCINLVGSYRCECRTGFIFNSISRSCEDIDECR-NYPGRLCAHKCENILGSY	397
Qy	189	SCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSD	247
Db	398	KCSCTAGFKLADDGRNCDDVNECES-SPCSQGCANVYGSYQSYCRRGYQLSDADGITCED	456
Qy	248	MDECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQT	304
Db	457	IDECALPTGGHICSYRCHNTPGSFHCTCPASGYTLAANGRSCQDIDECLTGTHSCSESES	516
Qy	305	CYNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGCRDQPFITILYRD	352
Db	517	CFNIQGGFRCLS-FDCPANYRRSGDTRPRVDRADIIRCVKSCQHNDISCVLNP--ILSHS	573

Qy 353 MDVVS-----GRSVPADIFQMATT-----RYPGAYYIFQIKSGNEGREFYMRQT---GP 399
: | : | : | : : | : | | : : |
Db 574 HTAISLPTFREFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSFDIIKRLDHGM 633

Qy 400 ISATLVMTRPIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
| : ||: || | | | | : : | : ||||| : : |
Db 634 IVGVVKQVRPLVGPVRTVLKLANNYVTNGVVSHR--NIINVRIYVSEFWF 681

Search completed: January 9, 2004, 12:34:05
Job time : 11.287 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:32:07 ; Search time 34.4615 Seconds
(without alignments)
3354.684 Million cell updates/sec

Title: US-09-674-379A-13
Perfect score: 2533
Sequence: 1 MPGIKRILTVTILALCLPSP.....INFRGSSVIRLRIYVSQYPF 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	1289	50.9	443	4	Q96TF5	Q96tf5 homo sapien
2	1283	50.7	443	11	Q9JM06	Q9jm06 mus musculu
3	1266	50.0	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1100	43.4	493	11	Q8BPB5	Q8bpb5 mus musculu
5	960.5	37.9	387	11	Q8K0J4	Q8k0j4 mus musculu
6	743	29.3	685	11	Q922K8	Q922k8 mus musculu
7	743	29.3	685	11	Q8C3B1	Q8c3b1 mus musculu
8	737	29.1	683	4	Q8TBH8	Q8tbh8 homo sapien
9	735.5	29.0	1174	11	Q99K58	Q99k58 mus musculu
10	728	28.7	598	6	Q8MJJ9	Q8mjj9 cercopithec
11	722	28.5	704	13	O73774	O73774 gallus gall
12	711.5	28.1	576	4	Q9Y3V7	Q9y3v7 homo sapien
13	710.5	28.0	1231	4	Q8IUI1	Q8iui1 homo sapien
14	709.5	28.0	1231	4	Q8IUI0	Q8iui0 homo sapien
15	696.5	27.5	638	4	Q8NBH6	Q8nbh6 homo sapien
16	676	26.7	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	631	24.9	681	13	O42182	O42182 brachydanio
18	587	23.2	698	5	Q9V4B8	Q9v4b8 drosophila
19	583	23.0	554	4	Q9UH16	Q9uh16 homo sapien
20	558.5	22.0	1409	5	Q9VS89	Q9vs89 drosophila
21	548	21.6	2673	4	Q96SC3	Q96sc3 homo sapien
22	537	21.2	5636	4	Q96RW7	Q96rw7 homo sapien
23	528.5	20.9	787	11	Q8K061	Q8k061 mus musculu
24	527.5	20.8	2872	11	Q9WUH8	Q9wuh8 rattus norv
25	524.5	20.7	741	4	Q96K89	Q96k89 homo sapien
26	522.5	20.6	1398	13	Q8AXM6	Q8axm6 xenopus lae
27	521.5	20.6	3857	11	O88840	O88840 mus musculu
28	521	20.6	1389	11	Q8CG18	Q8cg18 mus musculu
29	521	20.6	1713	11	Q8CG19	Q8cg19 mus musculu
30	520.5	20.5	1399	13	Q8JFZ4	Q8jff4 xenopus lae
31	519.5	20.5	2809	4	Q96JP8	Q96jp8 homo sapien
32	517	20.4	1713	11	O88349	O88349 mus musculu
33	516.5	20.4	708	13	P87363	P87363 gallus gall
34	515.5	20.4	2906	11	Q9WUH9	Q9wuh9 rattus norv
35	511.5	20.2	729	11	Q8BNH3	Q8bnh3 mus musculu
36	511.5	20.2	937	5	Q9BLJ1	Q9blj1 ciona intes
37	508	20.1	188	11	Q8R1U8	Q8rlu8 mus musculu
38	495.5	19.6	1963	6	Q28019	Q28019 bos taurus
39	495	19.5	746	4	Q96HB9	Q96hb9 homo sapien
40	495	19.5	893	6	Q8MJK0	Q8mjk0 cercopithec
41	495	19.5	1256	4	Q9NS15	Q9ns15 homo sapien
42	495	19.5	1382	4	Q9H7K2	Q9h7k2 homo sapien
43	494.5	19.5	1095	11	Q60784	Q60784 mus musculu
44	492.5	19.4	1764	11	O35806	O35806 rattus norv
45	491	19.4	517	4	Q9NP01	Q9np01 homo sapien

ALIGNMENTS

RESULT 1

Q96TF5

ID Q96TF5 PRELIMINARY; PRT; 443 AA.

AC Q96TF5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Mutant p53 binding protein 1 (MBP1).
 GN MBP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanka S.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tanaka S., Sugimachi K., Sugimachi K.;
 RT "Human mutant p53 binding protein (MBP1).";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB030655; BAA92880.1; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW EGF-like domain.
 SQ SEQUENCE 443 AA; 49421 MW; 9CE175F4F388A56D CRC64;

Query Match 50.9%; Score 1289; DB 4; Length 443;
 Best Local Similarity 49.9%; Pred. No. 7.4e-118;
 Matches 226; Conservative 74; Mismatches 131; Indels 22; Gaps 5;

QY 1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
 :|| : : :| | ||:: :||::| | | :|| |||||:|
 Db 8 LPGSLLLWALLLLLGSASPQDSEEPDSYTECTDGYEWDPSQHC RDVNECLTIPEACKG 67

 QY 56 DMMC VNQNGGYLCIPRTNPVYRGYPYSPYSGYPYAAAPPLSAPNYPTISRPLICRF 115
 :| |:| |||||:|:| :| : || | || | |
 Db 68 EMKCINHYGGYLCLPRSAVINDLHG-----EGP-PPVPVPAQHFN-----PCPP 111

 QY 116 GYQMDES NQCVDVDECATDSHCNPTQICINTEGGYTCSC TDGYWLLEGQCLDIDECRYG 175
 ||: |: : ||||| | | |:| | | | |:| ||| : :|:| |||||
 Db 112 GYEPDDQDSCVDVDECAQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171

 QY 176 YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
 ||| | |:| |:| :| | ||| : ||| |||| | | | |:| |:| |:| |
 Db 172 YCQHRCVNLPGSFRQCCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG 231

 QY 236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
 ||| || |||:| |:| :| |:| :| :| | | | | | | | | |
 Db 232 YELHRDGFSCSDIDECSSYLQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECESG 290

 QY 296 NHTCNLQQTTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPGCRDQPFITILYRDMDV 355
 | |: ||| | |:| |:| | | |||:| |:| | | |:| |:| |:| | :
 Db 291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSIVHRYMTI 350

QY 356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 415
 | | | | | | | : | | : | | : | | | | | | | : | | : | | : | | | |
 Db 351 TSERSVPADVFIQATSVPYGAAYNAFQIRAGNSQGDFYIRQINNVSAMLVLRPVTGP 410
 QY 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 | | | | | : | : | : | : | | | | : | | | |
 Db 411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443

RESULT 2

Q9JM06

ID Q9JM06 PRELIMINARY; PRT; 443 AA.
 AC Q9JM06;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 2.
 GN EFEMP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435063; PubMed=10982184;
 RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;
 RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
 RT from the multiple retinopathy critical region on 11q13.";
 RL Hum. Genet. 106:66-72(2000).
 DR EMBL; AF109122; AAF65189.1; -.
 DR HSSP; P00736; 1APQ.
 DR MGD; MGI:1891209; Efemp2.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW EGF-like domain; Matrix protein.
 SQ SEQUENCE 443 AA; 49452 MW; 5AEC2A91048B336A CRC64;

Query Match 50.7%; Score 1283; DB 11; Length 443;
 Best Local Similarity 49.9%; Pred. No. 2.9e-117;
 Matches 226; Conservative 70; Mismatches 135; Indels 22; Gaps 4;

QY 1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
 : | | : : | | : : : | | | : | | | | : | | | | : |
 Db 8 LPGSLLLWAFLLLLLGAASPDPEEPSYTECTDGYEWDADSQHCRDVNECLTIPEACKG 67
 QY 56 DMMCVNQNGGYLCIPRTNPVYRGYPYSPYSGPYPAAPPLSAPNYPTISRPLICRF 115
 : | | : | | | | : | | : : | | | | : | | |
 Db 68 EMKCINHYGGYLCIPRSAAVINDLHG-----EGPPPPAA-----HAQQPNPCPQ 111

QY 116 GYQMDESNOQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYG 175
 ||: || ||||| || ||: || || ||: ||| : :||:|||||
 Db 112 GYEPDEQESQVDECTQALHDCRPSQDCHNLPGSYQCTCPDGYRKIGPECVDIDECRYR 171
 QY 176 YCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
 ||| | |:| |: | ||| | : ||| ||||| || | |:| |:| |:| :
 Db 172 YCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCNQG 231
 QY 236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
 ||| || |||:| |:| |:| |:| |:| || ||| || | |||:| |
 Db 232 YELHRDGFSCSDIDECGYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECETG 290
 QY 296 NHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRIISDNRCMCPAENPGCRDQPFITILYRDMDV 355
 | |: ||| | ||:| |: | |||:| |||:| |||:| |||:| |||:| |:| :
 Db 291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYVQVSDNRCLCPASNPLCREQPSSIVHRYMSI 350
 QY 356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 415
 | ||||| |:| |:| |:| ||| |||:| |:| |:| |:| |:| |:| |:| |
 Db 351 TSERSVPADVFIQATSVYPGAYNAFQIRSGNTQGDYIRQINNVSAMLVLARPVTPG 410
 QY 416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
 ||||| |:| |:| |:| |:| |||:| |:| | |
 Db 411 YVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 443

RESULT 3

Q9H3D5

ID Q9H3D5 PRELIMINARY; PRT; 443 AA.
 AC Q9H3D5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin-like extracellular matrix protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seibold S., Marx M.;
 RT "Cloning of a new fibulin-like gene."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF124486; AAG45245.1; -.
 DR HSSP; P35555; 1EMN.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 3.
 DR PRINTS; PR00907; THRBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 5.
 KW EGF-like domain; Matrix protein.
 SQ SEQUENCE 443 AA; 49535 MW; D91784BF36A8A060 CRC64;

Query Match 50.0%; Score 1266; DB 4; Length 443;
 Best Local Similarity 49.2%; Pred. No. 1.3e-115;
 Matches 223; Conservative 74; Mismatches 134; Indels 22; Gaps 5;

```

Qy      1 MPGIKRILTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRG 55
          :|| : : :| | || ::: :||:|:| | | | :|| |||||:|
Db      8 LPGSLLLWALLLLLLLGSASPQDSEEPDSYTECTDGYEWDPDSSQHCRDVNECLTIPEACKG 67

Qy     56 DMMCVNQNGGYLCIPRTNPVYRGYPYSPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRF 115
          :| |:| |||||:|:| | : : || | || | | | |
Db     68 EMKCINHYGGYLCIPRSAAVINDLHG-----EGP-PPPVPPAQHPN-----PCPP 111

Qy    116 GYQMDENQCVDVDECATDSHQCNPTQICINTEGGYTCSCDTGYWLLLEGQCLDIDECRYG 175
          ||: |: : ||||| || | |:| | | | | |:| ||| : :|:| |||||
Db    112 GYEPDDQDSCVDVDECAQALHRRPSSQDCHNLGSGYQCTCPDGYRKIGPECVDIDECRYR 171

Qy    176 YCQQLCANVPGSYSCCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPG 235
          ||| | |:| |:| | | ||| | : ||| ||||| || | | |:| |:| |:| |
Db    172 YCQHRVCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCHQG 231

Qy    236 YELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHR 295
          ||| || |||:| |:| |:| |:| |:| |:| | | | | | | |:| |:|
Db    232 YELHRDGFSCSDIDECSSYLQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECESG 290

Qy    296 NHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDV 355
          | |: ||| | ||::|:| || |||::|:| |:| || | |:| |:| |:| | :
Db    291 AHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSIVHRYMTI 350

Qy    356 VSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 415
          | | |||:| |:| |:| ||| | |||:| | |:| | |:| |:| |:| |
Db    351 TSERMRPADVFQIQATSVYPGAYNAFQIRAGNSQGDYIRQINNVSAMLVLARPVTGP 410

Qy    416 IQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 448
          |||||:| |:|:|:| |||:| |:| | |
Db    411 YVLDLEMTMNSLMSYRASSVLRRLTVFVGAYTF 443
  
```

RESULT 4

Q8BPB5

```

ID  Q8BPB5      PRELIMINARY;      PRT;      493 AA.
AC  Q8BPB5;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Epidermal growth factor-containing fibulin-like extracellular matrix
DE  protein 1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Xiphoid cartilage;
RX  MEDLINE=22354683; PubMed=12466851;
RA  The FANTOM Consortium,
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
  
```

RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK077302; BAC36738.1; -.
SQ SEQUENCE 493 AA; 54952 MW; 9CEDC7BF2FF9430F CRC64;

Query Match 43.4%; Score 1100; DB 11; Length 493;
Best Local Similarity 42.0%; Pred. No. 2.8e-99;
Matches 206; Conservative 72; Mismatches 161; Indels 52; Gaps 6;

```
Qy      8 LTVTILALCLPSPGNAQ-----AQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ 62
      | :|:| | | | : | | | | | | | | | | | | | | | | | | | | | |
Db      5 LFLTMLTLALVKSQYTEETITYTQCTDGYEWDPIRQQCKDIDECDIVPDACKGGMKCVNH 64

Qy     63 NGGYLCIPRTNPFVYRGYPYSNPYSTPY-----GPYPAAAPP 98
      | | | | | :|:| | | | | | | | | | | | | | | | | | | | |
Db     65 YGGYLCLPKTAQIIVNNEHPQQETPAAEASSGATTGTVAARSMATSGVVPGGGFMASATA 124

Qy     99 LSAPNYPT-----ISRPLICRFGYQMDENQCVDDVDECATDSHC 138
      :|:| | | | | | | | | | | | | | | | | | | | | | | | |
Db    125 VAGPEVQVQGRNNFVIRNPADPQRI PSNPSHRIQCAAGYEQSEHNVQDIDECTSGTHNC 184

Qy    139 NPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFT 197
      | :| | | | | | | | | | | | | | | | | | | | | | | | |
Db    185 RTDQVCINLRGSFTCQCLPGYQKRGEQCVDIDECTVPPYCHQRCVNTPGSFYCQCSPGFQ 244

Qy    198 LNEDEGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFL 257
      | : : | :| | | | | | | | | | | | | | | | | | | | | |
Db    245 LAANNYTCVDINECDASNQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYL 304

Qy    258 CQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP 317
      | | :| | | | | : | | | | | : : | :| | | | | | | | | |
Db    305 CQYQCVNEPGKFSCMCPQGYEVV-RSRTCQDINECETTNE-CREDEMWNHGGFRICYPR 362

Qy    318 IRCEEPYLRI SDNRCMCPAENPGCRDQPFITLYRDMDDVSGRSVPADIFQMQATTRYPGA 377
      | :| : | :| | | | | | | | | | | | | | | | | | | | |
Db    363 NPCQDHYVLTSENRCVCPVSNMTCRELPQSIVYKYSIRSRSVPSDIFQIQATMIYANT 422

Qy    378 YYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVI 437
      | :| | | | | | | | | | | | | | | | | | | | | | | | |
Db    423 INTFRIKSGNENGEPYLRQTSFVSAMLVKLSLGPRIYIVDLEMLTVSSIGTFRFTSSVL 482

Qy    438 RLRIYVSQYPF 448
      | | | | : |
Db    483 RLTIIVGPFSF 493
```

RESULT 5

Q8K0J4

ID Q8K0J4 PRELIMINARY; PRT; 387 AA.
AC Q8K0J4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Qy 249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
 |||: :| :|:| ||| || :|:|:| || :|:|
 Db 485 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC 544
 Qy 306 YNLQGGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFITILYRDMDVVSGRSVPA 363
 :|:| |:|: ||| |:| || ||| :|:|:| || :|:|
 Db 545 FNIQGSFRCLS-FECPENYRRSADTRCERLPCHENQECPLPLRITYYHLSFPTNIQVPA 603
 Qy 364 DIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM- 422
 :|:| :|:| ||| :|:| ||| :|:|:| ||| :|:|:|
 Db 604 VVFRMGPSAVPGDSMQLAITAGNEEGFFTTRKVSHHSGVVALTKPIPEPRDLLLTVMKD 663
 Qy 423 -ITVNTVINFRGSSVIRLRIYVS 444
 || :| :|:|
 Db 664 LYRHGTVSSF----VAKLFIFVS 682

RESULT 7

Q8C3B1

ID Q8C3B1 PRELIMINARY; PRT; 685 AA.
 AC Q8C3B1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK086451; BAC39669.1; -.
 SQ SEQUENCE 685 AA; 75282 MW; E38377D35B08C560 CRC64;

Query Match 29.3%; Score 743; DB 11; Length 685;
 Best Local Similarity 36.1%; Pred. No. 4.1e-64;
 Matches 160; Conservative 65; Mismatches 154; Indels 64; Gaps 17;

Qy 16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPV 75
 || :|:| ||| :|:|:| ||| :|:| |||
 Db 290 CRP-----KLQCKSGFIQD-ALGNCIDINECLISAPCPVGQTCINTEGSYTC----- 336
 Qy 76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
 :|| :|:| :|:|:|:|:|
 Db 337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECSPP 365
 Qy 135 SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
 :| :|:| :|:| :|:|:| ||| :|:|:|:|
 Db 366 AEPCGKGHHCLNSPGSFRCKCKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFH 425

Qy 190. CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
 |:|: || |: |||||:||||| :|| | | |||: | | ||: | ||| | |:|
 Db 426 CSCSAGFRLSVDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 484
 Qy 249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
 |||: :| : |:| ||:: |||| | | : |:| |||:| | |:: :||
 Db 485 DECALPTGGHICSYRCINIPGSFQCSPPSSGYRLAPNGRNCQDIDECVTGIHNCSINETC 544
 Qy 306 YNLQGGFKCIDPIRCEEPLYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPA 363
 :|:| | |:| | | | | :| | | | | | : | : | | | |
 Db 545 FNIQGSFRCLS-FECPENYRRSADTRCERLPCHENQECPRPLRITYYHLSFPTNIQVPA 603
 Qy 364 DIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM- 422
 :|:| :| :| | :|| | | :| :| :|:| | |:: | :|
 Db 604 VVFRMGPPSSAVPGDSMQLAITAGNEEGFFTRKVVSHHSGVVALTKPIPEPRDLLLTVKMD 663
 Qy 423 -ITVNTVINFRGSSVIRLRIYVS 444
 || :| | :| | :||
 Db 664 LYRHGTVSSF----VAKLFIFVS 682

RESULT 8

Q8TBH8

ID Q8TBH8 PRELIMINARY; PRT; 683 AA.
 AC Q8TBH8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC022497; AAH22497.1; -.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 3.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 683 AA; 74423 MW; 2665A3961B6403B4 CRC64;

Query Match 29.1%; Score 737; DB 4; Length 683;
 Best Local Similarity 35.4%; Pred. No. 1.6e-63;

Matches 157; Conservative 67; Mismatches 154; Indels 66; Gaps 17;

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Qy      16 CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPV 75
      | |      : | | : | | | | : | |      | : | | | |
Db      288 CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----- 334

Qy      76 YRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATD 134
      : | |      | | | : | | : | | | | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPP 363

Qy      135 SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS 189
      : | |      | : | | : | | | | : | | : | : | | | |
Db      364 AEPCGKGHRCVNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYL 423

Qy      190 CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM 248
      | : | | | : | | | | : | | | : | | | | : | | : | | | |
Db      424 CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI 482

Qy      249 DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC 305
      | | | :      : | : | : | | | | | | : : | | | : | |
Db      483 DECALPTGGHICSYRCINIPGSFQCSCPSSGYRLAPNGSNQDIDECVTGIHNCSINETC 542

Qy      306 YNLQGGFKCIDPIRCEEPLYRISDNRC-MCPA-ENPGCRDQPFITILYRDMDVVSGRSVPA 363
      : | : | | | : | : | | | : | | | | | | : : | |
Db      543 FNIQGGFRCL-AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPA 601

Qy      364 DIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMI 423
      : | : | : : | | | | | | | | : | | : : | : | : | : :
Db      602 VVFRMGPPSSAVPGDSMQLAITGGNEEGFFTTRKVSPPHSGVVALTKPVPEPRDL-----LL 656

Qy      424 TVNTVINFRG--SSVIRLRIYVS 444
      | | : : | | | : | | |
Db      657 TVKMDLSRHGTVSSFVAKLFIFVS 680

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RESULT 9

Q99K58

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ID   Q99K58      PRELIMINARY;          PRT;  1174 AA.
AC   Q99K58;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to fibulin 2.
GN   FBLN2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005443; AAH05443.1; -.
DR   HSSP; P00736; 1APQ.
DR   MGD; MGI:95488; Fbln2.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR000152; Asx_hydroxyl.

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Query Match 29.0%; Score 735.5; DB 11; Length 1174;
Best Local Similarity 35.3%; Pred. No. 4.2e-63;
Matches 146; Conservative 61; Mismatches 148; Indels 59; Gaps 11;

```
QY      23 AQAQCTINGFDLDRQSGQLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSN 82
       |: :| :|| | | | :| :| :| :| :| :| :| :| :| :| :| :|
Db      782 ARQR CMDGF-LQDP EGN CVDIN ECTS LLEP CRSG FSCINT VGSYT C----- 826

QY      83 PYSTPYSGPYPA AAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPT 141
               ||:| || :| ::|||:| | | |:|
Db      827 -----QRNPLVCGRGYHANE EGSECVDVNECETGVHR CGEG 862

QY      142 QICINTEGGYTCSCTDG YW--LLEGQCLDI DECRYG---YCQQLCANVP GSY SCT CNPGF 196
       |:| | | | | | |: | :|::|| | | | | | | |:| ||
Db      863 QLCYNLP GS YRCDC KPGFQ RDAFGRTC IDVNECWVSP GR LCQHTCENT PG SYR CS CAAGF 922

QY      197 TLNEDGRSCQDVNECATENPCVQTCVN TYGSFI CRCDPGYE LEEDGVHCSDMDECS-FSE 255
       | ||: |:|||| | | | | | ||: | | ||:| || | |:|:||: :
Db      923 LLAADGKH CEDVNECETR -CSQE CANIYG SYQCYCRQGYQLA EDGHTCTDI DECAQGAG 981

QY      256 FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNH TCNLQQTCYNLQGGFKC 314
       || ||| ||:| |:|| || : : |||:|:| | | |: | :|:|:| |:|
Db      982 ILCTFR CVNVPGSY QCACPEQGYTMMANGRSCKDL DECALGTHNCSEAETCHNIQGSFRC 1041

QY      315 IDPIRCEE PYLRI SDNRC MCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQM 368
       : | | :|:|: :| | | :| | | : : :| ||| ||::
Db      1042 L-RFDCPP NYVRVSETKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHFRI 1096

QY      369 QATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLMVTRPIKGPREIQLDLEM 422
           : | | || | | |: : : :| : | | :|:|
Db      1097 GPAPAFA GD TISLTITKGNEEGYFVTRRLNAYTG VVSLORSVLEPRDFALD VEM 1150
```

08MJJ9

```

ID      Q8MJJ9      PRELIMINARY;      PRT;      598 AA.
AC      Q8MJJ9;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Fibulin-1c (Fragment).
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db 506 LSFPTNIQAPAVVFRMGPSAVPGDSMQLAITGGNEEGFFTTTRKVSPHSGVVALT KPVE 565

Qy 413 PREIQLDLEM--ITVNTVINFRGSSVIRLRIYVS 444
 ||:: | ::| || :| | :| ||::|

Db 566 PRDLLLTVKMDLYRHGTVSSF----VAKLFIFVS 595

RESULT 11

O73774

ID O73774 PRELIMINARY; PRT; 704 AA.
 AC O73774;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin-1, isoform D.
 GN FBLN1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120531; PubMed=9923656;
 RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
 RT "Identification of chicken and C. elegans fibulin-1 homologs and
 RT characterization of the C. elegans fibulin-1 gene.";
 RL Matrix Biol. 17:635-646(1998).
 DR EMBL; AF051399; AAC05387.1; -.
 DR HSSP; P00742; 1HCG.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 2.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;

Query Match 28.5%; Score 722; DB 13; Length 704;
 Best Local Similarity 34.6%; Pred. No. 4.8e-62;
 Matches 163; Conservative 68; Mismatches 158; Indels 82; Gaps 22;

Qy 15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP 70
 :| :||: : || || | | :||:| :| :| :|

Db 279 ICQNTFGSFRCRPKLQCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-Q 336

Qy 71 RTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMD-ENQCVDVD 129
 | :| | || :| :| |||

Db 337 RISP-----SCGRGYHLNEDGTRCVDVD 359

QY 130 ECATDSHCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRY---GYCQQLCANV 184
 ||:: | :|| | | | || :: |::||| | |
 Db 360 ECSSSDQPCGEGHVCINGPGNYRCECKSGYSFDVISRTCIDINECRYPGRGLCAHKCENT 419
 QY 185 PGYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGV 243
 |||| || | : ||||:|:| | : || | | |||: | | :| : ||:
 Db 420 PGSYCTCTMGFKLSSDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDGI 478
 QY 244 HCSDMDECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCN 300
 | |::|||: :| :| ||:: |::| | | : |::|||:| | | :
 Db 479 SCEDIDECALPTGGHICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCS 538
 QY 301 LQQTCYNLQGGFKCIDPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTI 348
 :||:|:|:|:|:|: : | | | : | | : | : | | |
 Db 539 FNETCFNIQGGFRCLS-LECPENYRKSGDTRVLEKTDTRICIKSCRPNVNCVLDPVHTI 597
 QY 349 LYRDMDVVSGRSV--PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTG 398
 : : : : | :| :| | | | | | | | | | | |
 Db 598 SHTVISLPTFREFTRPBEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DG 655
 QY 399 PISATLVMTRPIKGPRIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 448
 : ||| || | ||| : |:: | :: : |::| |
 Db 656 MTVGVVVRQVRPIVGPFHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF 704

RESULT 12

Q9Y3V7

ID Q9Y3V7 PRELIMINARY; PRT; 576 AA.
 AC Q9Y3V7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP586A1519.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL050095; CAB43267.1; -.
 DR HSSP; P00736; 1APQ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Hypothetical protein; EGF-like domain.
 FT NON_TER 1 1
 SQ SEQUENCE 576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;

Query Match 28.1%; Score 711.5; DB 4; Length 576;
 Best Local Similarity 34.3%; Pred. No. 4.1e-61;
 Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

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Qy      15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIP 70
      || : |: |:| :|| | | :||:| |:| | | |
Db      172 LCQNTKGSFYCQARQRCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC-- 228

Qy      71 RTNPVYRGPYSNPYSTPYSGPYAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD 129
      |||| | | |:| :|||:
Db      229 -----QRNPLICARGYHASDDGTKCVDVN 252

Qy      130 ECATDSHCNPTQICINTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANV 184
      || | |:| |:| | | | | | : |:|:| | | | |
Db      253 ECETGVHRCGEGQVCHNLPGSYRCCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENT 312

Qy      185 PGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH 244
      ||| |:| || | |:| :||| | : | | | | | |:| | | |
Db      313 LGSYRCSCASGFLLAADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT 371

Qy      245 CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ 302
      |:|:| |:| : || |:| |:| |:| | | : : |:|:|:| | | :
Db      372 CTDIDECAQAGILCTFRCLNVPGSYQCACEPQGYTMTANGRSCKDVDECALGTHNCSEA 431

Qy      303 QTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV 356
      |:|:| |:| |:| : | | |:| : | | | | | | | : :
Db      432 ETCHNIQGSFRCL-RFECPPNYVQVSKTKC----ERTTCHDFLECQNSPARITHYQLNFQ 486

Qy      357 SGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 416
      :| ||| |:|: : | | || | | : : : : | : |:|
Db      487 TGLLVPAHIFRIGPAPAFTGDTIALNIIKNEEGYFGTRRLNAYTGVVYLQRAVLEPRDF 546

Qy      417 QLDLEM 422
      ||:|
Db      547 ALDVEM 552
  
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RESULT 13

Q8IUI1

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ID   Q8IUI1          PRELIMINARY;          PRT; 1231 AA.
AC   Q8IUI1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Fibulin 2.
GN   FBLN2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li D., Marian A.J., Roberts R.;
RT   "Identification of a novel alternatively spliced isoform of human
RT   fibulin-2 gene abundantly expressed in heart and genetic evaluation in
RT   patients with ARVD.";
  
```

RL (In) Unknown A. (eds.);
 RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN
 RL GENETICS, pp.323-323, Unknown Publisher (2002).
 DR EMBL; AY130458; AAN05435.1; -.
 DR EMBL; AY130456; AAN05435.1; JOINED.
 DR EMBL; AY130457; AAN05435.1; JOINED.
 SQ SEQUENCE 1231 AA; 131853 MW; 0A75D1C27F258D48 CRC64;

Query Match 28.0%; Score 710.5; DB 4; Length 1231;
 Best Local Similarity 34.3%; Pred. No. 1.2e-60;
 Matches 146; Conservative 61; Mismatches 156; Indels 63; Gaps 12;

QY 15 LCLPSPGN---AQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIP 70
 || : |: |: |: || | | |: |: || :| || | | |
 Db 827 LCQNTKGSFYCQARQRCMDGF-LQDPEGNCVDINECTSLSEPCRPFGFSCINTVGSYTC-- 883
 QY 71 RTNPVYRGPYSNPYSTPYSGFYPAAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVD 129
 |||| || |: :|||:
 Db 884 -----QARNPLICARGYHASDDGXKCVDVN 907
 QY 130 ECATDSHQCNPTQICINTEGGYTCSTDTGYW--LLEGQCLDIDECRYG---YCQQLCANV 184
 || | |:| |:| | | | | |: |:|:| | | | |
 Db 908 ECETGVHRCGEGQVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENT 967
 QY 185 PGSYSCTCNPFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVH 244
 ||| |:| || | |:| |:| || | | | |:| | | | | |
 Db 968 LGSYRCSGASGFLAADGKRCEVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHT 1026
 QY 245 CSDMDECS-FSEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQ 302
 |:|:|:|: : || |:| |:| |:| || : : |:|:|:| | |
 Db 1027 CTDIDECAQGAGILCTFRCLNVPGSYQACPEQGYTMTANGRSCKDVDECALGTHNCSEA 1086
 QY 303 QTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVV 356
 |:|:|:| |:|: | |:| |:| | | | | | | : :
 Db 1087 ETCHNIQGSFRCL-RFECPPNYVQVSKTKC----ERTTCHDFLECONSPARITHYQLNLFQ 1141
 QY 357 SGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRI 416
 :| ||| |:| : | | | | |: : : : | : |
 Db 1142 TGLLVPAHIFRIGPAPAFTGDTIALNIIKNEEGYFGTRRLNAYTGVVYLQRAVLEPRDF 1201
 QY 417 QLDLEM 422
 ||:|
 Db 1202 ALDVEM 1207

RESULT 14

Q8IUI0

ID Q8IUI0 PRELIMINARY; PRT; 1231 AA.
 AC Q8IUI0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin 2.
 GN FBLN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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DE      Hypothetical protein NT2RP3003649.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA      Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA      Nagahari K., Sugano S., Isogai T.;
RT      "HRI human cDNA sequencing project.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AK075566; BAC11705.1; -.
DR      InterPro; IPR000020; Anaphylatoxin.
DR      InterPro; IPR000152; Asx_hydroxyl.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR006210; IEGF.
DR      Pfam; PF01821; ANATO; 1.
DR      Pfam; PF00008; EGF; 4.
DR      SMART; SM00181; EGF; 9.
DR      SMART; SM00179; EGF_CA; 9.
DR      PROSITE; PS00010; ASX_HYDROXYL; 4.
DR      PROSITE; PS01186; EGF_2; 3.
DR      PROSITE; PS01187; EGF_CA; 8.
KW      Hypothetical protein.
SQ      SEQUENCE      638 AA;  70577 MW;  EBC0DE3147A7621F CRC64;

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Qy	16	CLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGYLICI	PRTNPV	75
Db	223	CRP-----KLQCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC-----		269
Qy	76	YRGPYSNPYSTPYSGPYAAAPLSAPNYPTISRPLICRFGYQM-DESNOQVDVDECATD		134
Db	270	-----QKNVPN-----CGRGYHLNEEGTRCVDVDECAAPP		298
Qy	135	SHQCNPQTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYS		189
Db	299	AEPCKGKHRCVNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYL		358
Qy	190	CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDM		248
Db	359	CSCSVGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDI		417
Qy	249	DECSF--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTC		305
Db	418	DECALPTGGHICSYRCINIPGSFQCSCPSSGGYRLAPNGRNCQDIDECVTGIHNCSINETC		477
Qy	306	YNLQGGFKCIDPIRCEEPLYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDDVV		356
Db	478	FNIQGGFRCL-AFECPENYRISAATLQQEKTDTVRCI-----KSCRPNDDVTCVDFPVHTI		531
Qy	357	SGRSV-----PADIFOMOA-TTRYPG--AYYIFOIKSGNEGREF-----YMROTG		398

Search completed: January 9, 2004, 12:36:56
Job time : 36.4615 secs